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PERIPHERAL BLOOD CELL MARKERS USEFUL FOR DIAGNOSING  
MULTIPLE SCLEROSIS AND METHODS AND KITS UTILIZING SAME

FIELD AND BACKGROUND OF THE INVENTION

5           The present invention relates generally to the field of diagnosis, treatment assessment and prognosis. More specifically, the present invention relates to peripheral blood cell expressed markers and kits and methods utilizing same for diagnosing, treating and assessing the state of multiple sclerosis (MS) in an individual. The present invention also provides cellular  
10       markers which are useful in distinguishing between different clinical courses of MS e.g.: probable, relapsing-remitting, secondary progressive or primary progressive as well as response to the therapy.

          Multiple sclerosis is an autoimmune neurodegenerative disease, which is marked by inflammation within the central nervous system with lymphocyte  
15       attack against myelin produced by oligodendrocytes, plaque formation and demyelization with destruction of the myelin sheath of axons in the brain and spinal cord, leading to significant neurological disability over time. The disease frequently occurs in young adults between 20-40 years of age, is more prevalent in females than males (2:1), and has a characteristic geographical  
20       distribution – estimated prevalence in USA 120/100,000, (250,000 to 350,000 cases).

          The annual cost of MS in USA was estimated about \$34,000 per person, \$2.2 million total lifetime cost per case or \$6.8 billion yearly, in a conservative estimate of a national annual cost (Anderson DW, 1992; Whetten-Goldstain K.,  
25       1998).

***Clinical Diagnosis and Evaluation of Stages of MS***

          Typically, at onset an otherwise healthy person presents with the acute or sub acute onset of neurological symptomatology (attack) manifested by unilateral loss of vision, vertigo, ataxia, dyscoordination, gait difficulties,  
30       sensory impairment characterized by paresthesia, dysesthesia, sensory loss,

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urinary disturbances until incontinence, diplopia, dysarthria or various degrees of motor weakness until paralysis. The symptoms are usually painless, remain for several days to a few weeks, and then partially or completely resolve. After a period of remission, a second attack will occur. During this period after the first attack, the patient is defined to suffer from probable MS. Probable MS patients may remain undiagnosed for years. When the second attack occurs the diagnosis of clinically definite MS (CDMS) is made (Poser criteria 1983; C.M. Poser et al., Ann. Neurol. 1983;13, 227).

The clinical disease courses of MS are relapsing-remitting, primary or secondary progressive (Abramsky, 1997; Russell, 1998).

The relapsing-remitting course of MS (85% of patients) is characterized by acute attacks or relapses during which new neurological symptoms and signs appear, or worsen. Relapse develops within a period of several days, lasts for 6-8 weeks, then gradually resolves. During the acute relapse scattered inflammatory and demyelinating central nervous system (CNS) lesions produce varying combinations of motor, sensory, coordination, visual, and cognitive impairments, as well as symptoms of fatigue and urinary tract dysfunction. The outcome of a relapse is unpredictable in terms of neurological sequel but it is well established that with additional relapses, the probability of complete clinical remission decreases and neurological disability and handicap may develop. On average, about 60% of patients remain fully functional 10 years after the primary attack, and 25 to 30% remain fully functional 30 years after onset. Statistically, the disease does not greatly decrease life expectancy (mean decrease 12 years), although some patients become severely disabled and die from recurrent infections and complications.

Primary progressive MS (10% of patients) is characterized by slow, progressive neurological dysfunction usually in the form of a gradual myelopathy causing spasticity and ataxia. Treatment regimen varies greatly with different clinical course and severity of the disease.

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The diagnosis of MS is still defined primary by clinical terms and relies on a combination of history, neurological examination and ancillary laboratory and neuro-imaging studies.

Laboratory tests for MS include: 1) CSF evaluation of IgG synthesis, oligoclonal bands; 2) MRI of the brain and spinal cord and; 3) exclusion of other autoimmune diseases by blood tests [e.g.,; serum B12 level; HTLV 1 or HIV 1 titers; sedimentation rate or C-reactive protein; RA latex (Rheumatoid arthritis); ANA, anti-DNA antibodies (systemic lupus erythematosus)]. However, accurate diagnosis and prognosis in the “probable” stage, and early relapsing-remitting stages remains problematic. For example, it has been shown that positive MRI findings in the first demyelinating attack only provide a 50% successful prediction of development of clinically definite MS within 2-3 years (CHAMPS Study Group, *Neurology* 2002;59:998-1005). Likewise, Villar et al (*Neurology* 2002;59:877-83) found that detection of oligoclonal IgM bands with early symptoms were only partially predictive of development of clinically definite MS.

Other laboratory tests may provide some additional support for the diagnosis, but evidence of lesions disseminated in time and space remains a cardinal element of the diagnosis (Poser CM., 2001). In absence of definitive laboratory tests and pathognomonic clinical features, MS remains ultimately a diagnosis of exclusion.

Diseases that may be confused with MS are: 1) Acute disseminated encephalomyelitis (follows infections or vaccination mainly in children, fever, headaches, and meningitis common), 2) Lyme disease (antibodies to *Borrelia* species antigens in serum and CSF), 3) HIV associated myelopathy (HIV antibodies present), 4) HTLV I myelopathy (HTLV I antibodies present in serum/CSF), 5) Neurosyphilis (syphilis antibodies present in serum and/or CSF), 6) Progressive multifocal leukoencephalopathy (biopsy of lesions demonstrates virus by electron microscopy), 7) Systemic lupus erythematosus (CNS

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manifestations of lupus, antinuclear antibodies, anti-dsDNA), 8) Polyarteritis nodosa (systemic signs, micro-aneurysms demonstrated by angiographies, vasculitis demonstrated in biopsy of involved areas), 9) Sjogren's syndrome (dry eyes and mouth, antiRo and antiLa antibodies), 10) Behcet's disease (Oral/genital ulcers, antibodies to oral mucosa), 11) Sarcoidosis (CNS signs, increased protein in CSF, biopsy shows granuloma, 12) Paraneoplastic syndromes (older age group, antiYo antibodies), 13) Subacute combined degeneration of cord (peripheral neuropathy, vitamin B12 levels), 14) Sub acute myeloopticoneuropathy (adverse reaction to chlorhydroxyquinoline, mainly in Japanese), 15) Hereditary spastic paraparesis/ primary lateral sclerosis (normal CSF, MRI and visual evoked potential studies), 16) Adrenomyeloneuropathy (adrenal dysfunction, neuropathy, increased plasma very long-chain fatty acids), 16) Spinocerebellar syndromes (familial, pes cavus scoliosis, abnormal reflexes, normal CSF IgG), 17) Miscellaneous – strokes, tumors, arteriovenous malformations, arachnoid cysts, Arnold-Chiari malformations, and cervical spondylosis all may lead to diagnostic dilemmas on occasion. Thus, detailed history and neurological examination must be complemented by specific laboratory tests for the correct diagnosis of MS. Clearly there is a long felt need for more powerful diagnostic tools for prediction and staging of MS.

***Etiology of MS***

The etiology of MS is unknown. It is suggested that a combination of genetic background and environmental factors and immune response are involved in the disease. A certain incidence of familial occurrence has been observed, with the concordance rate among monozygotic twins being 30%, a 10-fold increase over that in dizygotic twins or first-degree relatives (Steinman, 1966; Dymment et al Mol. Gen 1997;6:1693-98). In addition, recent research indicates that the tissue damage in MS occurs as the result of pathological autoimmune responses to several myelin antigens following exposure to an as yet undefined environmental causal agent.



However, although some environmental factors have been statistically associated with the disease, none have provided correlations of any predictive value. Environmental factors seem to trigger MS in subjects who are already genetically susceptible to the illness. Most probably no one dominant gene determines genetic susceptibility, but rather many genes, each with different influence, are involved. Indeed, the initial pathogenic process could be caused by one group of genes, while others groups could be responsible for the development and progression of the disease (Oksenberg, 2001; Compston, 1997).

#### *Microarray Analysis and MS*

Microarray technology is based on hybridization of mRNA to high-density array of immobilized target sequences. Each sequence corresponds to a specific gene(s) of interest. The labeled pool of sample mRNA is subsequently hybridized to the array (chip). Application of this technology provides the capability of monitoring thousands of various genes simultaneously. Today commercial available DNA microarrays (Affymetrix, Santa Clara CA, USA) contain elements representing 10,000, 20,000 or more genes that have been characterized in terms of function or disease association. The preparation and use of microarrays for diagnostics, research and drug development is disclosed in, inter alia, US Pat. Nos. 6,324,497 and 6,468,476 to Friend et al and 6,410,229 to Lockhart et al; and Intl Pat. Application WO 0053625C2 and A2.

Several application of microarrays in human disease have been reported, for example the identification (marker) genes involved in ovarian carcinogenesis (Ono K., 2000); classification of genes expression profiling of cutaneous malignant melanoma (Bitter M., 2000); and expression profile of Tangl-Rearing CA1 neurons in Alzheimer's disease (Stephen, 2000). Alizaden (2000) characterized gene expression in diffuse large B cell lymphoma, where two distinct gene expression patterns, characterized by different molecular forms of B cells lymphoma, were identified. In addition, microarray

technology has also been applied to diagnosis and monitoring of such diverse diseases as cancer (US Pat. No. 6,511,849 to Freuhauf et al), psoriasis (Intl Pat. Application WO 20020027538 to Trepicchio et al), T-helper cell related diseases (Trepicchio et al , Intl Pat Application WO 20020039734), Epstein-Barr disease (U.S. Pat. Nos. 6,506,553 and 6,468,476 to Smith and Parks), rheumatoid arthritis (Intl Pat Application WO 0248310A2 to Trepicchio et al) and Reward Deficiency Syndrome, all of which are incorporated herein by reference.

In a recent review (Greenberg SA., 2001) the author discussed the potential application of DNA microarray technology for understanding neurological disorders. Using cDNA microarrays technology, brain tissue from pathology lesions and normal white matter of single MS patient were analyzed (Whitney LW.,1999). Blood genomic fingerprints were demonstrated after experimental strokes, seizures, hypoglycemia and hypoxia of rats (Yang Tang, 2001). Similarly, microarray analysis of gene expression in brainstem and spinal cord tissues from the animal models of MS (experimental autoimmune encephalomyelitis, EAE) has identified a number of differentially expressed genes from active-acute versus silent lesions (Lock C. et al Nat Med 2002;8,500-504), and also suggested a role for the proinflammatory cytokine osteopontin in the development of EAE in mice (Chabas D et al Science 2001;294:1731-34).

In another recent study, Ramanathan M et al (J of Immunology 2001;116:213-19) used cDNA microarray technology to identify abnormal gene expression patterns in PBMC of relapsing-remitting MS patients. The study compared PBMC gene expression in 15 patients during remission (only) with that of 15 healthy controls, using a GeneFilters GF211 array (Research Genetics, Huntsville AL, USA) having approximately 5200 human gene sequences. Groups of marker genes correlated with MS were disclosed, but the range of differences (fold changes) between level of gene expression in MS and

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control groups was only 13 to 35 % for unregulated and from 11 to 43% for down regulated genes. Such small differences are probably due to the limited sensitivity of the technology employed in using GeneFilters arrays, and may not have any clinical or diagnostically mining significance. More significantly, the population of MS patients was limited, including only patients during clinical remission, who had not received any immunosuppressive treatment for at least 3 months. Thus, the markers described do not provide a profile of expression patterns useful for diagnosing clinically defined MS in patients having probable MS, or for determining stages of the disease.

Trepicchio et al. (Intl Pat. Application No. WO 02/079218 A1) also describe the use of microarray technology in determining characteristic gene expression in an animal model of MS (murine EAE) and in tissue samples from MS patients. The human samples were PBMC or brainstem tissue, collected from 60 patients manifesting a wide variety of symptoms, at different stages of MS including relapsing-remitting, primary and secondary progressive, and acute exacerbation. RNA probes prepared from these samples were hybridized to a human chip array containing approximately 14,000 gene sequences (MicroArray, Affymetrix, cat no. 510448, Santa Clara CA), and expression profiles compared with those of healthy controls. Determination of the panel of “MS-related” markers was based merely on fold change of greater than 2 fold (up- or downregulated), with a confidence level of  $p < 0.01$ . No more stringent statistical criteria were applied. A “panel” of 300 differentially regulated genes was thus described in the PBMC samples, and another 100 in the brain lesion tissue. However, no classification of expression profiles characteristic to specific stages of the disease was provided, and the “class predictor model”, as described, using “neighborhood analysis”, was applied for attempted prediction of “MS-afflicted” or “non-diseased” samples only. Thus, the panel of markers described is not applicable to the diagnosis of stage of MS, in general, is

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unsuited for the prediction of clinically definite MS or probable MS patients, and is clearly non-predictive in monitoring response to treatment.

There is thus a widely recognized need for, and it would be highly advantageous to have gene expression profiles useful in distinguishing between different forms of MS e.g.: probable, relapsing-remitting, primary or secondary as well as response to the therapy, devoid of the above limitations.

SUMMARY OF THE INVENTION

According to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising determining a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below a method of monitoring a state of multiple sclerosis in a subject, the method comprising monitoring a level of expression of at least one gene selected from the group consisting of the genes listed in Tables I-V over a predetermined time period, wherein substantial difference between the levels of expression of the at least one gene over the predetermined time period indicates a change in a state of the multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below monitoring the level of expression of at least one gene over the predetermined time period is effected by periodically obtaining a sample from the individual and determining the level of expression of the at least one gene in the sample.

According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes

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each independently selected from the group consisting of the genes listed in Tables I-V.

According to another aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis, the method comprising the step of determining a level of expression of each of the genes listed in Tables I-V in a sample obtained from the subject, wherein a substantial difference between expression levels of the genes in the sample obtained from the subject and normal expression levels of the genes is an indication that the subject is afflicted with multiple sclerosis.

According to further features in preferred embodiments of the invention described below the normal expression level of the at least one gene or genes is determined by measuring the level of expression of the gene or genes in at least one control sample obtained from at least one healthy individual.

According to still further features in the described preferred embodiments the sample includes peripheral blood mononuclear cells.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of  $p=0.05$  as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample. According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.

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According to an additional aspect of the present invention there is provided a method of assessing the efficacy of a treatment regimen on multiple sclerosis in a subject, the method comprising determining a level of expression of at least one gene or genes selected from the group consisting of the genes listed in Tables I-V in samples obtained from the subject prior to, and following exposure to the treatment regimen, wherein a substantial difference in the expression level of at least one gene or genes between the samples is an indication that the treatment regimen is efficacious in treating multiple sclerosis in the subject.

According to further features in preferred embodiments of the invention described below the treatment regimen is administering at least one test compound for inhibiting multiple sclerosis.

According to still further features in the described preferred embodiments the treatment regimen is an environmental condition.

According to yet further features in the described preferred embodiments the substantial difference is a difference statistically significant at a confidence level of  $p=0.05$  as determined by at least one test selected from the group consisting of a t-test, a TNoM and an INFO score.

According to further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes is determined by quantifying a level of a protein product thereof in the sample.

According to still further features in the described preferred embodiments quantifying a level of the protein is effected using a reagent which specifically binds with the protein.

According to yet further features in preferred embodiments of the invention described below the reagent comprises an antibody or fragments thereof.

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According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table III.

According to further features in preferred embodiments of the invention described below the at least one gene or genes are selected from the genes listed in Table IV.

According to still further features in the described preferred embodiments at least one gene or genes are selected from the genes listed in Table V.

According to yet further features in preferred embodiments of the invention described below the level of expression of the at least one gene or genes in the sample is determined by detecting the presence in the sample of a transcribed polynucleotide or portion thereof. The transcribed polynucleotide can be mRNA.

According to further features in preferred embodiments of the invention described below the transcribed polynucleotide or portion thereof is detected via a labeled probe which specifically hybridizes with the transcribed polynucleotide or portion thereof.

According to still further features in the described preferred embodiments the sample from a subject is T cells, the at least one gene or genes are selected from the genes listed in Table IV and the normal expression of the gene or genes is T-cell expression.



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According to still further features in the described preferred embodiments the at least one gene comprises at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in  
5 Tables I-V.

According to another aspect of the present invention there is provided a kit for diagnosing multiple sclerosis in a subject, the kit comprising components suitable for determining expression levels of at least one gene selected from the group of genes listed in Tables I-V.

10 According to further features in the described preferred embodiments the reagents include at least one polynucleotide sequence selected capable of specifically hybridizing with an transcription product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one polynucleotide sequence and said transcription product.

15 According to still further features in the described preferred embodiments the reagents include at least one antibody selected capable of specifically binding a polypeptide product of the at least one gene and reagents for detecting and optionally quantifying a complex formed from the at least one antibody and the polypeptide product.

20 According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table I.

According to still further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed  
25 in Table II.

According to yet further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table III.

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According to further features in preferred embodiments of the invention described below the at least one gene is selected from the genes listed in Table IV.

According to still further features in the described preferred  
5 embodiments at least one gene is selected from the genes listed in Table V.

According to further features in preferred embodiments of the invention described below the kit further comprises packaging material identifying the kit as useful from diagnosing MS.

According to another aspect of the present invention there is provided a  
10 polynucleotide array comprising at least 10 and no more than 1500 polynucleotide sequences, wherein each of the sequences is selected capable of hybridizing with a transcription product of a polynucleotide sequence of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention  
15 described below the array is selected having polynucleotide sequences capable of diagnosing subjects suspected of suffering from multiple sclerosis. The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention  
20 described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

According to yet another aspect of the present invention there is provided an array comprising at least 10 and no more than 1500 antibodies or  
25 antibody fragments each capable of specifically binding a protein product of a gene selected from the group of genes listed in Tables I-V.

According to further features in preferred embodiments of the invention described below the array is selected having antibodies or antibody fragments capable of diagnosing subjects suspected of suffering from multiple sclerosis.

The subjects may also be suspected of suffering from probable multiple sclerosis, primary progressive multiple sclerosis, secondary progressive multiple sclerosis, and/or relapsing/remitting multiple sclerosis.

According to further features in preferred embodiments of the invention  
5 described below the gene is selected from the genes listed in Table I, II, III, IV and/or IV.

Implementation of the method and system of the present invention involves performing or completing selected tasks or steps manually, automatically, or a combination thereof. Moreover, according to actual  
10 instrumentation and equipment of preferred embodiments of the method and system of the present invention, several selected steps could be implemented by hardware or by software on any operating system of any firmware or a combination thereof.

#### 15 BRIEF DESCRIPTION OF THE DRAWINGS

The invention is herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of the preferred  
20 embodiments of the present invention only, and are presented in the cause of providing what is believed to be the most useful and readily understood description of the principles and conceptual aspects of the invention. In this regard, no attempt is made to show structural details of the invention in more detail than is necessary for a fundamental understanding of the invention, the  
25 description taken with the drawings making apparent to those skilled in the art how the several forms of the invention may be embodied in practice.

In the drawings:

FIGs. 1A-B are graphic representations of the differences in PMBC gene expression between MS patients and healthy subjects. RNA from Peripheral

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Blood Mononuclear Cells (PMBC) of 26 patients diagnosed with MS, and 18 healthy, age-matched controls was purified, labeled hybridized to a Genechip array (U95Av2, Affymetrix Inc. Santa Clara CA, USA), scanned and analyzed according to manufacturer's recommendations. The data were normalized and fold ratios calculated for each gene of the MS samples against the geometric mean of the controls. Figure 1A shows the number of MS specific genes detected having increased expression (fold change greater than 1.5) analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% ( $p=0.10$ ) to 100% ( $p=0$ ). Note the high level of significant MS-related gene expression at 95% FDR and above (arrows) (1249 distinguished genes). Figure 1B is an infogram of the 1249 genes most significantly ( $p<0.05$  on all three tests) distinguishing MS patients (MS) from (control) healthy controls, determined as above. Each spot represents expression of a specific gene; color intensity of overexpressed (green) and under-expressed (red) genes indicates fold increase as compared to controls. Gray color indicates genes showing no difference in expression between MS and controls.

FIGs. 2A-B are graphic representations of the differences in PMBC gene expression between MS patients during acute relapse, and MS patients in remission. RNA from PMBC of 12 relapsed, and 14 clinically in remission patients was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Figure 2A shows the number of acute relapse-specific genes detected having increased expression in relapse, as analyzed by t-test (red line), TNoM (green line) and INFO (blue line), compared with random occurrence (black line), at confidence levels (False Discovery Rates, FDR) of 90% ( $p=0.10$ ) to 100% ( $p=0$ ). 735 genes were detected having significant relapsing-related gene expression at 95% FDR and above. Figure 2B is an infogram analysis of the 735 genes most significantly ( $p<0.05$  on all three tests) distinguishing acute relapsing MS patients (Relapse) from MS patients in

remission (Remission). Note the different profiles of gene expression in patients undergoing treatment (Relapse + and Remission +) compared with untreated patients (Relapse- and Remission -).

FIG. 3 is a pie chart diagram showing the breakdown, by functional character, of specific genes displaying up- or down-regulation in MS-derived MOG-reactive T-cell lines, as compared to normal-derived MOG-reactive T-cell lines. Significant MOG reactive MS-related genes are defined as genes with TNoM=0 and  $p=0.057$  as compared to normal MOG-reactive T-cells.

FIG. 4 is a graphic representation of the differences in gene expression between MOG-stimulated T-cell lines from MS patients and healthy controls. RNA from MOG-stimulated T-cells of 4 MS patients and 3 matched controls was purified, labeled, hybridized and analyzed as described for Figures 1A-B hereinabove. Panel A shows a cluster analysis of 150 differentially expressed genes analyzed as described hereinabove (TNoM=0,  $p<0.05$ ) distinguishing T-cells of MS (MS) patients from controls (Controls). Panel B shows a cluster analysis of the 43 most informative genes (TNoM=0,  $p<0.05$ , and fold change  $>1.5$ ). Each row represents a gene, and each column represents a T-cell line from a different subject. Yellow color indicates genes with an increased expression relative to controls are yellow, and blue color indicates genes with relative decreased expression.

#### DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention is of methods and kits for diagnosing multiple sclerosis in subjects, using novel gene expression profiles derived from peripheral blood cells. Specifically, the present invention can be used to diagnose MS in early stages of the disease, to determine clinical stage and predict the course of the disease in patients with a unclear diagnoses, to provide definition and prognostic information in patients with probable MS, to assess

and monitor MS therapies and to screen new and established drugs and treatments for MS.

The principles and operation of the present invention may be better understood with reference to the drawings and accompanying descriptions.

5        Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangement of the components set forth in the following description or illustrated in the Examples and drawings. The invention is capable of other embodiments or of being practiced or carried out  
10 in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

The present invention provides previously unavailable accuracy in predicting and staging MS, by identifying genes and groups of genes  
15 specifically over- and under-expressed in PBMC of patients at various stages of their disease.

As is further described in the Examples section which follows, the present inventors have conducted a broad scale analysis of PMBC expressed genes using hybridization of biotin-labeled PBMC mRNA to more than 12,000  
20 human gene sequences provided on DNA chips. By utilizing specialized statistical analysis approaches, the present inventors identified in the microarray data the most highly informative expression profiles.

As mentioned hereinabove, multiple sclerosis is a chronic, multi-factorial neurodegenerative disease of unknown etiology, the diagnosis and  
25 classification of which remains largely clinical in nature. Identification of the stages and progression of the disease, particularly definition of the probable MS stage, is crucial to determination of optimal treatment regimen and development of effective therapies. However, the complexities of autoimmune interactions, and the variability of MS in different individuals have made diagnosis and

subsequent prognosis using traditional methods inexact and challenging. Methods for more accurate diagnosis of MS are greatly needed.

The profiles of MS-related genetic markers listed in Table I represent genes exhibiting differential expression in PBMCs from a large sample of MS patients, compared to that of age-matched healthy controls. Abundance of specific gene transcripts, represented by the intensity of label hybridizing to individual sequence loci of the MicroArray (Affymetrix Inc, Santa Clara CA), was recorded and quantified according to the manufacturers recommended protocols (such as GeneChip 3.0 software from Affymetrix). However, rather than composing the profile of differentially expressed genes based on probabilities using simple distribution of mean intensities, as has been reported by Ramanathan et al (J Immunol 2001;116:213-219), informative genes were selected based on the degree to which they were predictive of classification of the sample as “diseased” or “not diseased”. By applying the rigorous three-pronged statistical analysis described in detail hereinbelow, 1249 genes most informative in distinguishing between diseased and otherwise not diseased patients were identified (see Table I). By applying an even more restrictive analysis of the data in Table I (see Table II, Bonfferoni analysis), a subset of the 300 highest scoring genes was identified. These MS marker genes comprise both over-expressed and downregulated genes, and represent of a diverse group of functional gene categories. Additional analysis of the markers uncovered herein also led to the identification of another restricted marker set which can be accurately utilized to diagnose probable MS patients. As is further described hereinbelow, the identification of such a marker set represents a significant breakthrough since it enables to treat individuals at a much earlier stage of MS then previously possible.

Thus, according to one aspect of the present invention there is provided a method of diagnosing a subject with multiple sclerosis by determining a level of expression of at least one gene of the genes listed in Tables I-V in a sample

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obtained from the subject, wherein a substantial difference between the level of expression of the gene in the sample obtained from the subject and a normal expression level of the gene is an indication that the subject is afflicted with multiple sclerosis.

5        Normal expression levels of a marker or markers are obtained from isolated or cultured PMBCs (e.g., T-cell cultures), or samples obtained from individuals not affected with MS. A substantial difference is preferably of a magnitude that is statistically significant (see the Examples section for more detail). In particularly preferred embodiments, the marker is increased or  
10        decreased relative to control samples by at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, or 10-fold or more. Similarly, one skilled in the art will be well aware of the fact that a preferred detection methodology is one in which the resulting detection values are above the minimum detection limit of the methodology utilized.

As is further described in the Examples section which follows, the  
15        marker listed in Tables I-V were identified in peripheral blood cells. As such, the sample obtained from the individual is preferably a peripheral blood sample or any sample which includes blood cells such as T-cells. In a preferred embodiment, the sample is blood, thymus, spleen, lymph, pus, or bone marrow. However, it will be apparent to one skilled in the art that PMBCs may be  
20        present as an infiltrate in many other tissues, and that such tissues may also serve as samples in which the presence, activity, and/or quantity of the markers of the invention may be assessed. The tissue samples containing one or more of the markers themselves may be useful in the methods of the invention, and one skilled in the art will be well aware of methods by which such samples may be  
25        conveniently obtained, stored, preserved and processed. For further description relating to collection and processing of blood samples please see the Examples section which follows.

As is detailed in the Examples section below, analysis of PBMC genes differentially expressed in MS, according to the methods described herein,



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revealed groups of genes of specific interest in MS. Genes that are most significantly over expressed, or downregulated in MS can indicate members of pathways important to disease development or pathology. Strongly overexpressed genes, according to Tables I and II, include **SLAM** (signaling lymphocyte activation molecule, GenBank Accession No. U33017), **LEF1** (lymphoid enhancer-binding factor 1, GenBank Accession No. AL099409), **LRP5** (low density lipoprotein receptor-related protein 5, GenBank Accession No. AF077820), **LILRB** (leukocyte immunoglobulin-like receptor, GenBank Accession No. AF004230), **LY75** (lymphocyte antigen 75, GenBank Accession No. AF011333), **CDW52** (GenBank Accession No. N90866), **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma, GenBank Accession No. AB011161), **MAP4** (Microtubule-associated protein 4, GenBank Accession No. M64571), **CTSK** (Cathepsin K, GenBank Accession No. X82153) and **CTSB** (Cathepsin B, GenBank Accession No. L22507).

Strongly down-regulated genes include **IL1B** (Interleukin 1 beta, GenBank Accession No. M15330), **TRAF6** (GenBank Accession No. U78798), **SCYA20** (GenBank Accession No. U64197), **IL1R** (type1 receptor, GenBank Accession No. M27492), **IL1RAP** (receptor accessory protein, GenBank Accession No. AB006537) and **IL1RN** (receptor antagonist, GenBank Accession No. X52015), **TGFB1** (Transforming growth Factor beta 1, GenBank Accession No. X05839), **SKI** (v-ski sarcoma viral oncogene homologue, GenBank Accession No. X15218), **VEGF** (Vascular endothelial growth factor, GenBank Accession No. M63978), **IGFBP4** (Insulin-like growth factor binding protein 4, GenBank Accession No. U20982), **EREG** (epiregulin, GenBank Accession No. NM\_001432.1), and **NR4A1**, **NR4A2**, **NR4A3** (nuclear receptor family genes, GenBank Accession Nos. NM\_002135.1, X75918 and U12767, respectively).

Functional groups of genes strongly represented in the profile of most significantly differentially regulated genes in MS include, inter alia, apoptosis-

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related genes, T-cell activation and expansion related genes, cell proliferation related genes and epidermal growth factor genes. Many of the marker genes identified are associated with other MS- related genes, according to Tables I-V.

It will be appreciated that although a single marker can be used for diagnosis, diagnostic accuracy typically increases with an increase in the number of markers utilized.

As such, the diagnostic method of the present invention preferably utilizes a marker set that can range anywhere from 2 genes to 1200 genes. For example, the present method can utilize at least 10, at least 50, at least 100, at least 250, at least 500, at least 750, at least 1000 or at least 1200 genes each independently selected from the group consisting of the genes listed in Tables I-V. Most preferably the markers utilized are selected from the sequences listed in Table II.

The markers sets utilized can be selected according to a statistical significance or fold change thereof (provided for each marker in Tables I-V), a higher significance and higher fold change indicating higher probability of marker accuracy. For example, a selected marker set can encompass markers displaying a high statistical significance (low P-value), preferably a P-value lower than  $5.0E-02$ , more preferably lower than  $5.0E-04$ , most preferably, lower than  $5.0E-06$ . Alternatively, markers can be selected according to shared features of the marker gene. For example, gene markers of similar cellular function (e.g., genes of a signaling pathway such as apoptosis) or markers displaying similar activity (e.g., enzymes of the same enzyme family) can be grouped into specific marker sets.

Each marker set may be considered individually, although it is within the scope of the invention to provide combinations of two or more marker sets for use in the methods and compositions of the invention to increase the confidence of the analysis.

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As used herein, the terms "polynucleotide" and "oligonucleotide" are used interchangeably, and include polymeric forms of nucleotides of any length, either deoxyribonucleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform  
5 any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment, exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers.

10 A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by  
15 conjugation with a labeling component. The term also includes both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of this invention that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

20 As used herein, a "gene" includes a polynucleotide containing at least one open reading frame that is capable of encoding a particular polypeptide or protein after being transcribed and translated. Any of the polynucleotide sequences described herein may be used to identify larger fragments or full-length coding sequences of the gene with which they are associated. Methods  
25 of isolating larger fragment sequences are known to those of skill in the art, some of which are described herein. A "gene product" includes an amino acid (e.g., peptide or polypeptide) generated when a gene is transcribed and translated.

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As used herein, a "probe" is defined as an oligonucleotide that is provided as a reagent to detect a target present in a sample of interest by hybridizing with the target. Usually, a probe will comprise a label or a means by which a label can be attached, either before or subsequent to the hybridization reaction. Suitable labels include, but are not limited to radioisotopes, fluorochromes, chemiluminescent compounds, dyes, and proteins, including enzymes.

As used herein, "expression" includes the process by which polynucleotides are transcribed into mRNA and translated into peptides, polypeptides, or proteins. "Differentially expressed", as applied to a gene, includes the differential production of mRNA transcribed from a gene or a protein product encoded by the gene. A differentially expressed gene may be overexpressed or underexpressed as compared to the expression level of a normal or control cell. In one aspect, it includes a differential that is 2.5 times, preferably 5 times or preferably 10 times higher or lower than the expression level detected in a control sample. The term "differentially expressed" also includes nucleotide sequences in a cell or tissue which are expressed where silent in a control cell or not expressed where expressed in a control cell.

As used herein, the term "polypeptide" is defined as a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits may be linked by peptide bonds. In another embodiment, the subunit may be linked by other bonds, e.g., ester, ether, etc. As used herein the term "amino acid" includes either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics. A peptide of three or more amino acids is commonly referred to as an oligopeptide. Peptide chains of greater than three or more amino acids are referred to as a polypeptide or a protein.

As used herein, the term "marker" is defined as a polynucleotide or polypeptide molecule which is present or absent, or increased or decreased in

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quantity or activity in subjects afflicted with multiple sclerosis, or in cells involved in multiple sclerosis. The relative change in quantity or activity of the marker is correlated with the incidence or risk of incidence of multiple sclerosis or progression from one stage of the disease to another.

5        Although all of the markers listed in Tables I-V can be used in diagnosis of MS, an additional object of the present invention was to identify those markers which can be utilized to diagnose specific clinical forms and/or stages of MS.

10        Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable.

As a result of comprehensive studies conducted in efforts to evaluate specific gene expression in relation to clinical disease phases, the present invention provides, for the first time, specific markers sets which can be utilized in accurate diagnosis of specific forms and stages of MS

15        As is illustrated in Example II of the Examples section which follows, the present invention provides marker sets which can be accurately utilized to diagnose acute relapse, remission and probable stages of MS (Tables III-V).

Of particular importance is the marker set provided in Table V. As is described in the Examples section which follows, the present inventors also  
20        uncovered cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity. Although MS appears to be caused by autoimmune T-cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of  
25        great clinical and investigational importance.

Cellular markers which distinct between disease-related and non-disease related T-cell myelin reactivity include down-regulating apoptosis associated genes, up regulating anti-apoptotic genes and genes responsible for increased expansion capability of autoreactive T cells and enhanced ability to penetrate

the CNS. Thus, the markers of Table V include genes involved in perpetuating pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. This marker set accurately defines the requirements for an individual to develop MS, and thus has important predictive value, especially in diagnosing individuals having MS in the "probable" stage.

The identification of these markers significantly advances the field of MS diagnosis and treatment as well as provides tools which will enable elucidation of the mechanisms underlying MS formation and progression, ultimately leading to formulation of efficient, stage specific, treatment regimens.

The markers of the invention may be nucleic acid molecules (e.g., DNA, cDNA, or RNA) or the polypeptides encoded thereby. As such, detection of markers in a sample obtained from an individual can be effected using various detection methods well known to the ordinary skilled artisan.

Briefly, measurement of the relative amount of nucleic acid or polypeptide molecules can be effected by any method known in the art (see, e.g., Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992). Typical methodologies for RNA detection include RNA extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., a complementary nucleic acid molecule) specific for the target RNA to the extracted RNA, and detection of the probe (e.g., Northern blotting). Typical methodologies for polypeptide detection include activity assays in cases of known enzymes, protein extraction from a cell or tissue sample, followed by hybridization of a labeled probe (e.g., an antibody) specific for the target protein to the protein sample, and detection of the probe. The label group can

be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Detection of specific polypeptide and nucleic acid molecules may also be assessed by gel electrophoresis, column chromatography, direct sequencing, or quantitative PCR (in the case of nucleic acid molecules) among many other techniques well known to those skilled in the art.

Probes based on the nucleotide sequence of a marker gene or of a nucleic acid molecule encoding a marker polypeptide of the invention can be used to detect transcripts or genomic sequences corresponding to the marker gene(s) and/or marker polypeptide(s) of the invention. In preferred embodiments, the probe comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress (e.g., over- or under-express) a marker polypeptide of the invention, or which have greater or fewer copies of a marker gene of the invention. For example, a level of a marker polypeptide-encoding nucleic acid in a sample of cells from a subject may be detected, the amount of mRNA transcript of a gene encoding a marker polypeptide may be determined, or the presence of mutations or deletions of a marker gene of the invention may be assessed. The invention further encompasses nucleic acid molecules that differ from the nucleic acid sequences of the genes set forth in Tables I-V, due to degeneracy of the genetic code and which thus encode the same proteins as those encoded by the genes shown in Tables I-V.

An isolated marker protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind marker proteins using standard techniques for polyclonal and monoclonal antibody preparation. A full-length marker protein can be used or, alternatively, the invention provides antigenic peptide fragments of these proteins for use as immunogens. The antigenic peptide of a marker protein comprises at least 8 amino acid residues of an amino acid sequence encoded by a gene set forth in Tables I-V, and

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encompasses an epitope of a marker protein such that an antibody raised against the peptide forms a specific immune complex with the marker protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the marker protein that are located on the surface of the protein, e.g., hydrophilic regions, as well as regions with high antigenicity.

An anti-marker protein antibody (e.g., monoclonal antibody) can be used to isolate a marker protein of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-marker protein antibody can facilitate the purification of natural marker proteins from cells and of recombinantly produced marker proteins expressed in host cells. Moreover, an anti-marker protein antibody can be used to detect marker protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the marker protein. Anti-marker protein antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase,



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luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (J. Mol. Biol. 1990;215:403-10). BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to marker protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

It will be appreciated that non-coding sequences, such as promoter or other regulatory sequences of marker genes may be used as probes in the context of the present invention. Thus, the expression of groups of functionally related genes, responsive to similar signals important to the pathogenesis or progression of multiple sclerosis, may be assessed.

It will be appreciated that in certain cases the genes themselves can serve as markers. For example, mutations in the nucleic acid sequence of a gene (e.g., non-sense, mis-sense deletion and the like) which result in lower expression levels of the gene or lower activity of the gene product may be correlated with MS. Similarly, a duplication of the gene, which can result in higher expression levels or mutations which result in higher activity can also be correlated with MS.

Detection of the presence or number of copies of all or a part of a marker gene of the invention may be performed using any method known in the art. Typically, it is convenient to assess the presence, quantity and quality of genomic DNA by Southern analysis, in which total DNA from a cell or tissue sample is extracted, is hybridized with a labeled probe (e.g., a complementary DNA molecule), and the probe is detected. The label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Other useful methods of DNA detection and/or quantification include direct sequencing, gel electrophoresis, column chromatography, and quantitative PCR, as is known by one skilled in the art.

In cases where detection involves discrete marker sets, the detection method of the present invention preferably employs marker probes which are conjugated to a solid support. For example, polynucleotide probes capable of specifically hybridizing with polynucleotide markers of the present invention (e.g., mRNA) may be coupled to an array (e.g., a GeneChip array for hybridization analysis), to a resin (e.g., a resin which can be packed into a column for column chromatography), or a matrix (e.g., a nitrocellulose matrix for northern blot analysis). The immobilization of molecules complementary to the marker(s), either covalently or noncovalently, permits a discrete analysis of the presence or activity of each marker in a sample. In an array, for example, polynucleotides complementary to each member of a marker set may individually be attached to different, known locations on the array (region-specific arrays). The array may be hybridized with, for example, polynucleotides extracted from a blood sample obtained from a subject. The hybridization of polynucleotides extracted from the sample with the array at any location on the array can be detected, and thus the presence or quantity of the marker in the sample can be ascertained. In a preferred embodiment, a "GeneChip" array is employed (e.g., an Affymetrix type array). Similarly, Western analyses may be performed on immobilized antibodies specific for

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different polypeptide markers hybridized to a protein sample from a subject.

It will also be apparent to one skilled in the art that the probes of the array need not bind with the entire marker molecule. A probe designed to bind a portion of the marker of sufficient length for detection purposes (e.g., for hybridization), for example, a portion of the marker which is 7, 10, 15, 20, 25,  
5 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 100 or more nucleotides or amino acids in length may be sufficient for detection purposes.

Polynucleotide probes can be synthesized using any known synthesis method. Preferably, synthesis is effected using on-chip lithography methodology in a manner similar to that utilized for the synthesis of Affymetrix  
10 chips ([www.affymetrix.com](http://www.affymetrix.com)). Additional methods of array production and methodology are described in detail in the U.S. Patent Applications cited in the Background section hereinabove.

Antibody probes useful for detecting polypeptide markers can be generated using various well known techniques. For example, monoclonal  
15 antibodies which can be used per se or as a basis for antibody fragments (scFv, Fab etc) can be synthesized using isolated Hybridomas. In such an approach, a protein corresponding to a marker of the invention is isolated (e.g., by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein in vivo or in vitro using  
20 known methods. A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the  
25 vertebrate exhibits a robust immune response to the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened

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using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the protein or protein fragment.

The invention also includes an array comprising a marker(s) of the present invention. The array can be used to assay expression of one or more genes in the array.

In one embodiment, the array can be used to assay gene expression in a tissue of multiple sclerosis patients at different stages of the disease to ascertain stage specificity of genes in the array. In this manner, more than about 30,000 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more stages of the disease.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only stage specificity, but also the level of expression of a battery of stage specific genes is ascertainable. Thus, genes can be grouped on the basis of their expression per se, and level of expression in that stage of the disease.

The detection arrays described herein are preferably packaged in kits identified for use in detecting MS in general or for detecting specific stages of MS. The kit can further include reagents suitable for the detection of polynucleotide hybridization or antibody binding and instructions for effecting diagnosis using the kit components and suitable detection hardware (e.g., detection microscope) and software (e.g., detection and analysis software). For further description of such hardware and software and detection reagents please see [www.affymetrix.com](http://www.affymetrix.com).

Thus, the present invention provides methods useful for diagnosing MS including specific stages or states of the disease and also a risk of developing the disease.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells), detecting the presence, quantity, and/or activity of one or

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more markers of the invention in the sample relative to a normal sample. Observing a significant increase or decrease in one or more markers in the test sample indicates the presence or risk of presence of MS.

Using specific marker sets, the present invention also provides methods  
5 of assessing the severity or stage of MS in a subject.

As detailed hereinabove, a major concern in treatment of multiple sclerosis is accurate early diagnosis following the first acute attack. At present, clinical studies indicate that only 40-50% of individuals suffering a first acute attack will progress to clinically definite MS. Thus, treatment protocols most  
10 commonly suspend treatment of these patients defined as probable MS, until the appearance of a second attack, which may entail years of waiting and uncertainty. It will be appreciated that early and accurate detection of the portion of probable MS patients likely to progress to further stages of the disease can save undue suffering and expense, and, more importantly, provide  
15 early treatment and a better prognosis for the portion of probable MS patients likely to progress to more severe stages. The present invention provides, for the first time, marker genes for probable MS, as well as for relapsing vs. remitting MS.

The present invention also provides methodology which can be used to  
20 assess the efficacy of an MS treatment regimen and/or the effect of environmental factors or diet on the progression of MS.

These methods involve isolating a sample from a subject (e.g., a sample containing T-cells) suffering from MS who is undergoing treatment which includes drug therapy, exposure to a predetermined environmental condition  
25 and/or a specific diet, detecting the presence, quantity, and/or activity of one or more markers of the invention in test samples obtained from the subject prior to and following treatment or in a test sample obtained from the subject relative to a sample obtained from an individual suffering from MS who is not undergoing any treatment and/or relative to a sample obtained from an individual not

suffering from MS and undergoing treatment. The levels of markers in the samples are compared, and significant increases or decreases in one or more markers in the test sample following treatment relative to the other samples are observed, and correlated with the severity or stage of MS. By assessing whether  
5 MS has been lessened or alleviated, the ability of the treatment or therapy to treat MS is also determined.

It will be appreciated that the present invention also provides methods of treating (e.g., inhibiting) the formation or progression of MS. These methods involve isolating a sample from a subject (e.g., a sample containing PMBCs  
10 such as T-cells), detecting the presence, quantity, and/or activity of one or more markers of the invention in the sample relative to a normal sample and observing significant increases or decreases in one or more markers in the test sample. For markers that are significantly decreased in expression or activity, the subject may be administered that expressed marker protein, or may be  
15 treated by the introduction of mRNA or DNA corresponding to the decreased marker (e.g., by gene therapy), to thereby increase the levels of the marker protein in the subject. For markers that are significantly increased in expression or activity, the subject may be administered mRNA or DNA antisense to the increased marker (e.g., by gene therapy), or may be administered antibodies  
20 specific for the marker protein, to thereby decrease the levels of the marker protein in the subject. In this manner, the subject may be treated for MS or MS related condition.

In another embodiment, the methods further involve obtaining a control biological sample (e.g., nondiseased tissue) from a control subject, contacting  
25 the control sample with a compound or agent capable of detecting marker protein, mRNA, or genomic DNA, such that the presence of marker protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of marker protein, mRNA or genomic DNA in the control sample

with the presence of marker protein, mRNA or genomic DNA in the test sample.

The invention also provides methods for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (e.g., stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (e.g., peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker. The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; (see, e.g., Zuckermann et al., 1994, J. Med. Chem. 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145).

Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon

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examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

5

**EXAMPLES**

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures  
10 utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current  
15 Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998);  
20 methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Culture of Animal Cells - A Manual of Basic Technique" by Freshney, Wiley-Liss, N. Y. (1994), Third Edition; "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al.  
25 (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578;



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3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345;  
4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide  
Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D.,  
and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D.,  
5 and Higgins S. J., eds. (1984); "Animal Cell Culture" Freshney, R. I., ed.  
(1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical  
Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology"  
Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And  
Applications", Academic Press, San Diego, CA (1990); Marshak et al.,  
10 "Strategies for Protein Purification and Characterization - A Laboratory Course  
Manual" CSHL Press (1996); all of which are incorporated by reference as if  
fully set forth herein. Other general references are provided throughout this  
document. The procedures therein are believed to be well known in the art and  
are provided for the convenience of the reader. All the information contained  
15 therein is incorporated herein by reference.

**MATERIALS AND METHODS**

**Subjects** - Blood was obtained from patients or controls after written  
informed consent. *For comparison of healthy controls and MS patients, and*  
20 *between MS patients in acute relapse or remission:* Gene expression profiles of  
26 patients (20 females, mean age  $41.0 \pm 2.5$  years) with definite diagnosis of  
MS according to Poser criteria (8), a relapsing-remitting disease course, and  
brain magnetic resonance imaging ascertaining the diagnosis (9) were  
compared with eighteen (18) age-matched healthy subjects (16 females). *For*  
25 *comparison of transcriptional profiles in MOG-reactive T-cells:* Four MS  
female patients (mean age  $38 \pm 4.2$  years, mean disease duration  $9.3 \pm 3.3$  years)  
having a definite MS according to Poser criteria (10), a relapsing-remitting  
disease course, neurological disability evaluated by the expanded disability  
status scale (EDSS, 11) between 2 to 5.0, and brain MRI supporting the

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diagnosis of MS, and three age- and sex-matched healthy controls were included in the study. None of the patients received immunomodulatory drugs or steroid treatment for at least three months prior to when blood was drawn. The studies were approved by the institutional review board and the Israel  
5 Ministry of Health.

**mRNA preparation** - Total RNA was isolated from Ficoll™ isolated Peripheral Blood Mononuclear Cells (PBMC) or from MOG-stimulated T cell lines ( $2 \times 10^7$  cells) by ice-cold TRIZOL Reagent (Gibco, BRL). Poly-A mRNA was isolated using a mini-kit (Oligotex, Qiagen) and used as a template for  
10 double-stranded cDNA synthesis using oligo (dT)-24 primers containing a T7 RNA polymerase promoter site added to the 3'- end (Genset). After phenol/chloroform extraction cDNA was used as a template for *in vitro* transcription (Ambion T7 Megascript system) with biotin labeled nucleotides (Enzo Diagnostics). Labeled cRNA was fragmented, quantified by  
15 spectrophotometer, and hybridized to the microarrays.

**Microarray gene analysis** - Each Genechip (U95Av2) which carries probes for 12,625 (or U133A with 22,000 for patients with probable MS diagnosis) transcripts was hybridized with 10µg/200µl hybridization mix, stained and scanned (Hewlett Packard, GeneArray-TM scanner G2500A)  
20 according to manufacturer protocol (Affymetrix Inc, Santa Clara, CA). Scaling procedure was performed to an average intensity of 600 per gene. A value of 20 was assigned to all measurements lower than 20. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission:* All data was normalized by dChip software and fold ratios were  
25 calculated for each gene of the samples against geometric means of the matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells:* Genes that did not have at least one average difference intensity value  $\geq 100$  or were present at least once by Affymetrix criteria, were not included in the analysis.

**Data analysis** - The analysis was performed according to the analytical approach as previously described (24-26). Genechip 4 software (Affymetrix Inc, Santa Clara, CA) was used for analysis of the scanned arrays. Fold ratios were calculated for each gene of the samples against the geometric mean of matched controls. *For comparison of transcriptional profiles in MOG-reactive T-cells:* To determine the most informative genes threshold number of misclassifications (TNoM) score was applied. This score counts the number of classification errors that occur between compared groups for each gene of the dataset. The best threshold (TNoM=0) implies that no errors have been counted and the distinction between the two groups in relation to the expression level of a specific gene is maximal. To select a group of strongly differential expression, t-test p-value (comparing expression levels of genes from MS patients vs. healthy controls) were also computed. Genes with TNoM = 0, fold-change >1.5 (either up or down regulated) and corresponded t-test P value < 0.05, were designated as most informative. *For comparison of healthy controls and MS patients, and between MS patients in acute relapse or remission:* The data was analyzed by the classic parametric t-test, and the following non-parametric tests: (i) Threshold number of misclassifications (TNoM) method and (ii) INFO score that measures the misclassifications made by a simple threshold in terms of the information lost. Analysis was performed between MS patients and the control group for each gene of the dataset as well as between subgroups of patients. Only informative MS related genes ( $p < 0.05$  in all three statistical tests) were included. To retrieve the most informative genes, the False Discovery Rate (FDR) method (14) that ranks and tests all “P” values against different thresholds was used. The degree of significance by the Bonferroni threshold method, which evaluates the allowed error probability divided by the number of genes measured, and ensures that each and every validated scoring event is indeed a significant event, was also calculated.

***Validation Strategy*** - To further assess the predictive power of the data sets, computerized analysis by the Leave-One-Out-Cross-Validation (LOOCV) statistical method was performed. The method simulates removal of a single sample every trial and trains on the rest. The procedure is repeated until each sample is left out once and the number of correct and incorrect predictions is counted.

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**EXAMPLE I**

***Accurate Gene Expression Profiles of MS***

In order to provide an accurate, reliable profile of gene markers for diagnosis and evaluation of MS, DNA chip analysis was used to compare multiple gene expression patterns of PBMCs from patients with different clinical forms of MS. After informed consent blood was obtained from 26 patients (20 females, mean age 41.0±2.5 years) with definite diagnosis of MS according to Poser criteria, a relapsing-remitting disease course, and brain magnetic resonance imaging ascertaining the diagnosis. Eighteen age-matched healthy subjects (16 females) served as controls. PBMC gene expression of 12,625 human genes was analyzed as described hereinabove, using Ficoll™ for preparation of PBMCs and total RNA purification and sample preparation according to the instructions of Affymetrix, Inc (Affymetrix, Santa Clara CA, USA). In order to determine the most informative genes, unique computerized scoring methods, as yet not applied to analysis of data regarding MS, were employed. In brief, a gene is designated as informative based on the degree to which its tissue expression level is predictive of an independent classification of the tissue sample as “diseased” or “not diseased”, as previously described by Ben-Dor et al (J Comput Biol 2000;7:559-63) and applied to the analysis of breast cancer and melanoma using cDNA arrays (for review see Freidman N et al Ernst Schering Res Found Wkshp 2002;38:109-31). The scores used in this study were:

***TNoM (Total Number of Misclassifications)*** - the number of classification errors committed when using the best simple threshold to distinguish between two classes (diseased or not diseased) based on the expression levels of a specific gene.

***INFO*** - an estimate of the uncertainty remaining about accuracy of a sample classification (diseased or not diseased) after the incorporation of

predictions based on expression of an individual gene is given (a lower “INFO” score indicates a higher predictive value for a given gene).

***Gaussian (t-test)*** - The overlap between distributions of expression levels for genes in two classes. The score is based on normality assumptions.

5 One of the advantages of the analytic methods used here is their amenability to rigorous statistical benchmarking. Using this unique analysis, the number of informative genes per score expected in a random classification can be calculated, and then this estimated number of high scoring (or informative) genes can be compared to the actual number of informative genes  
10 (per score) measured in a dataset.

Comparison of the gene expression profiles shows that gene expression of PBMC in MS patients is significantly different from that in healthy subjects. Under the null-hypotheses that the separation of the samples is random despite genetic heterogeneity between tested groups, observed significant  
15 overabundance of informative genes was observed (Fig. 1A). The difference between expected and observed number of genes with significant p value in all 3 statistical tests (t-test, TNoM, INFO) performed, indicates that the diversity in gene expression observed in PBMC is biologically significant.

The predictive power of the data sets results was assessed by performing  
20 computerized error estimates based on *leave-one-out cross validation* (LOOCV) trials. The results disclosed only 3 classification errors. This low rate of error estimates suggest that the gene expression signature in MS is reliable for the diagnosis of the disease using peripheral blood and confirms that the patterns we observed accurately represent significant biologic phenomena  
25 associated with MS. The false discovery rate (FDR) method distinguished 1249 most informative genes that pass 95% FDR on all three statistical tests (t-test, TNoM, INFO) at  $p < 0.05$  (Fig. 1B and Table I).

Confirmation of gene microarray expression findings was performed by RT-PCR for the following five randomly selected genes: EGFL5, P44, GS3686,

MX1 and CCR2. Significant correlations (coefficients ranged from 0.76 to 0.98) were found between the relative number of expression genes analysis and the RT-PCR profile. The data from microarray hybridizations was further tested against the strict Bonferroni threshold method from all three statistical tests, as described hereinabove, resulting in 300 top scoring genes that distinguish between MS and healthy subjects. (Table II).

The 1249 most informative genes (681 up-regulated, 569 down-regulated, Table I) consist of inflammatory, apoptosis and cell signaling pathways components, cytokines, antigen presentation molecules and chemokines as well as number of expressed sequence tags (ESTs).

***Over-expressed genes in MS*** - The most abundant over-expressed transcripts unique to MS include: (i) **SLAM** (signaling lymphocyte activation molecule) a member of the immunoglobulin gene superfamily that is involved in T-cell stimulation. SLAM potentiates T-cell expansion and was described as CD28 independent co-stimulatory molecule, selectively increasing interferon gamma production and dysregulating type 1 and type 2 cytokine production in MS upon T-cell receptor activation. The surprising observation of SLAM upregulation suggests an enhanced proliferation of autoreactive T cells in MS patients; (ii) **LEF1** (lymphoid enhancer-binding factor 1) one of the transcriptional factors expressed in pre-B and T cells, and known to be associated with T cell receptor (TCR) stimulation and apoptosis survival of pro-B cells (19); (iii) **LRP5** (low density lipoprotein receptor-related protein 5) a of cell receptor protein required for LEF1 activation; (iv) **LILRB** (leukocyte immunoglobulin-like receptor), a protein that binds MHC class I molecules and delivers a negative signal inhibiting killing by natural killer and regulatory T cells; (v) **LY75** (lymphocyte antigen 75) an endocytotic receptor used by dendritic cells to direct captured antigens from the extracellular space to a specialized antigen-processing compartment; and (vi) **CDW52**, a 21-28 kDa glycopeptide antigen expressed on lymphocytes and macrophages known to be

a target for complement-mediated insult, inducing pro-inflammatory cytokine (e.g. TNF alpha and interferon gamma) production. Other up-regulated genes are members of the anti-apoptotic pathways, and include **PIP5K1-gamma** (Phosphatidylinositol-4-phosphate 5-kinase, type 1, gamma) and **MAP4** (Microtubule-associated protein 4). Over-expression of transcripts belonging to the papain cysteine proteinase family **CTSK** (Cathepsin K) and **CTSB** (Cathepsin B) was also observed.

*Down-regulated genes in MS* - Abundant down-regulated transcripts unique to MS that were identified include **IL1B** (Interleukin 1 beta), an important inflammatory cytokine; **TRAF6**, which is essential for IL1 signaling; and **SCYA20**, known to be mediated by IL1B. Decreased mRNA expression of **IL1B** was strengthened by the down regulation of **IL1R** (type1 receptor), **IL1RAP** (receptor accessory protein) and **IL1RN** (receptor antagonist).

Other important down-regulated genes include **TGFB1** (Transforming growth Factor beta 1) and **SKI** (v-ski sarcoma viral oncogene homologue) a component of TGFB signaling pathway, both known to inhibit cell proliferation. Thus, their under expression may contribute to autoreactive T cell expansion. Members of epidermal growth factor family such as **VEGF** (Vascular endothelial growth factor), **IGFBP4** (Insulin-like growth factor binding protein 4) and **EREG** (epiregulin) were also down regulated. Additionally, mRNA expression of members of the steroid-thyroid receptors family including nuclear receptor subfamily 4, group A members 1, 2 and 3 (**NR4A1**, **NR4A2**, **NR4A3**) were significantly reduced. Down regulation of these genes may inhibit apoptosis through Fas ligand and tumor necrosis factor alpha or through early response of T-cell receptor induced apoptosis of thymocytes, thus mimicking positive selection.

Taken together, the identification of profiles of up- (overexpressed) and down regulated genes specific to MS indicates the suitability of the methods of the present invention for identifying validated and significant molecular



signatures of PBMC gene expression in MS. While reducing the present invention to practice, it was observed that the specific disease related genes include transcripts involved in T cell activation and expansion and anti-apoptotic mediators, indicating failure of apoptosis-related elimination of autoreactive T cells.

## EXAMPLE II

### *Stage Specific Gene Expression Profiles of MS*

Accurate clinical tools for specific diagnosis of disease stages in MS are presently unavailable. In order to provide a useful profile of the clinically defined stages of MS, specific gene expression was evaluated in relation to clinical disease phases. Significant overabundance was found between the number of observed and expected genes expressed in MS patients during an acute relapse and in remission (Fig. 2A). Using the methods described hereinabove, the 743 most informative genes (302 up-regulated and 441 down-regulated) with p-value < 0.05 in all three scores (t-test, TNoM, INFO) that differentiated relapse from remission (Fig 2B, Table III) were identified.

***Over-expressed genes in acute relapse of MS, compared to patients in remission*** - The most informative over-expressed genes included CTSL (Lysosomal cystein protease L, cathepsin L) known to play a role in MHC class II antigen presentation, responsible for quantitative and qualitative difference in peptide repertoires displayed by MHC class II molecules, and having a regulatory role in epitope generation for antigens subsets. Moreover, in vitro, proteolytic CTSL processed myelin basic protein into more than 60 different 20-40-mers species, and myelin-associated glycoprotein was described as a substrate for CTSL like proteases. These data, taken together with our observation that CTSL mRNA was over expressed in the active stage of MS, offer a biochemical basis for the immunodominant epitope spreading implicated in the pathogenesis of MS. Also up-regulated is SCYA2 (Monocyte

specific chemoattractant protein, MCP1), essential for monocyte and NK cells recruitment to site of inflammatory injury. Augmented SCYA2 expression level in the CNS has been identified at the onset of EAE. Other abundant up-regulated transcripts identified by the method of the present invention include  
5 **CD79A**, **DDIT3** (DNA-damage inducible transcript 3); **E2-EPF** (Ubiquitin carrier protein) and **COX6**.

*Downregulated genes in acute relapse of MS, compared to patients in remission* - From the downregulated gene transcripts in acute relapse vs. remission it is important to note several programmed cell death-related genes  
10 like **CCNG1** (Cyclin G1) identified as p53 dependent apoptosis; **PDCD2** (Programmed cell death 2) expressed in immature thymocytes; and **CTLA1** (Cytotoxic T lymphocyte associated serine esterase 1), crucial for the rapid induction of apoptosis by cytotoxic cells. Also prominently downregulated during acute relapse was **JAK1** (Janus kinase 1), a protein tyrosine kinase  
15 reported to be obligatory for several cytokines receptors, important for regulation of acute cellular response.

The results of the functional annotation of the transcriptional motifs that distinguish between acute MS relapse and remission suggest that many of the genes are involved in cellular recruitment and epitope spreading, as well as  
20 important to immunologic mechanisms related to escape from regulatory surveillance and augmentation of cell survival potential. Thus, it can be suggested that during the acute inflammatory process of the disease there is a failure of the immune regulatory cells to inhibit autoreactivity and the self-expansion of the non-restrained autoreactive T cells further lead to a vicious  
25 cycle of on going inflammatory activity.

It is evident from the gene-clustering map (Fig 2B) that during an acute relapse no significant differences are found between relapse treated vs. relapse untreated patients. Such a result is of great clinical significance, since this may indicate that during an acute MS exacerbation the major gene expression

transcripts are related to relapse associated genes and the effect of therapy is negligible. However, during remission treatment effect was more pronounced and this effect on gene suppression in treated patients was evident.

Of even greater significance is the demonstration, for the first time, of a specific gene expression profile of the “probable” stage of MS. As described hereinabove, “probable” MS precedes definitive clinical diagnosis, and is characterized by diverse neurological symptoms including unilateral loss of vision, true vertigo, ataxia, paresthesia, incontinence, diplopia, dysarthria or paralysis. Probable MS patients may suffer undiagnosed for years. In order to provide a method for accurate diagnosis of probable MS, in advance of onset of clinical symptoms, gene expression in PBMC samples of 13 probable MS patients were compared with that of samples from 5 age-matched healthy controls. RNA preparation, hybridization to MicroArray and analysis of results was performed as described for Examples 1 and 2, and in the Material and Methods section hereinabove.

As is shown in Table V, a specific “probable” MS profile of gene expression distinguishes PBMCs of diseased and healthy individuals.

Thus, there is demonstrated, for the first time, gene expression profiles providing criteria for distinguishing between stages of MS in humans, for example, between relapsing and remitting MS, probable MS and healthy individuals. Further, the groups of up- and down-regulated genes identified herein may be used for investigation of mechanisms of disease and disease progression in MS.

### **EXAMPLE III**

#### ***Gene Expression Profiles in Treatment of MS***

The effect of immunomodulatory treatment on gene expression in MS patients was investigated by comparison analysis of gene transcripts between treated and untreated patients. Surprisingly, despite the variety of

immunomodulatory treatments and differences between patients in relation to treatment duration, the microarray methods described herein, treatment-related gene transcripts that differentiated between treated and untreated patients were detected. Treatment-specific gene expression is mainly associated with phosphorylation and signal transduction. Thus, gene microarray technology can be a powerful tool in evaluating and monitoring clinical correlations of effects of treatment, and determining prognosis.

Thus, data presented herein demonstrate for the first time distinct and significant fingerprint cluster in MS patients that differentiates them from healthy subjects. Moreover, the stringent and specific fingerprint is predictive for the diagnosis of MS and is suitable for guiding the selection of patients for early treatment. Additionally, separate gene expression patterns were identified between acute MS relapse and remission, and treatment effects could also be identified. The methods described herein may also be used to offer superior insight into the biological mechanisms involved in the disease as well as improving functional gene characterization and transcription sites detection, important for identification of new targets for treatment and drug identification, such as T cell activation and expansion and anti-apoptotic genes like **SLAM**, **PIP5K1-g** and the **NR4A1-3** steroid-thyroid receptors subfamily.

#### ***EXAMPLE IV***

##### ***Gene Expression Profiles of MOG-Reactive T-cells from MS Patients***

Although MS appears to be caused by autoimmune T cells activated against myelin self-antigens, myelin-reactive T-cells have been demonstrated in healthy subjects as well. Thus, distinction between disease-related and non-disease related T-cell myelin reactivity is of great clinical and investigational importance. In order to determine a profile of MS-related T-cell genes, gene expression in MOG-reactive T-cells from 4 MS patients having relapsing-

remitting disease course, positive Poser criteria, and neurological disability, and 3 healthy age-matched controls was compared.

Using the microarray methods described herein, gene expression patterns obtained in MOG reactive T cell lines from MS patients detected 150 transcripts with  $TNoM=0$ ,  $p=0.057$  compared to healthy subjects (Figure 4). These high scoring gene transcripts were defined as significant MOG reactive MS-related genes. Hierarchical clustering of gene expression patterns from MS patients and healthy controls is presented in Figure 2, panel A. From the 150 genes with absolutely different expression levels, 43 most informative genes were further identified and clustered. These include 18 up-regulated and 25 down-regulated genes (Figure 2, panel B).

Investigation of the known biological function of these genes (Table V) shows a great diversity of activity (A Pie-chart diagram showing the functional groups of genes included in this evaluation is presented in Figure 3). Included are genes coding for proteins involved in the regulation and execution of apoptosis, growth factors, mediators of signal transduction pathways, molecules that participate in inflammation and also genes encoding heat shock proteins, transcription factors and components of different biochemical pathways.

*Upregulated Genes in MS-Derived T-cells* - Up-regulated in MS patient-derived T-cell lines are several anti-apoptotic genes such as **BCL2**, **lifeguard**, and the MAP-activated kinase **MAP3K12**. The **BCL2** gene product is an important member of the anti-apoptotic proteins. Lifeguard (**LFG**), is a molecule that inhibits cell death mediated by the Fas (CD95) receptor through a unique mechanism that down regulates apoptotic signals from Fas and is associated with human autoimmune lymphoproliferative syndrome (ALPS) and in lymphoproliferative lupus-like syndrome in mice.

The **MAP3K12** gene is associated with programmed cell death and encodes a polypeptide that catalyzes the phosphorylation of **BAD**, a member of the **BCL2** anti-apoptosis protein family. Increased expression of **IGFBP3** and

**VEGF** was also demonstrated in MS-derived T cells. **IGFBP-3** has been implicated in the expansion of disease related T-cell, associated with acute brain lesions of MS patients. Thus, in addition to increased survival potential, our findings suggest that autoreactive T cells in MS also have an expansion advantage compared with T cells from healthy individuals.

Furthermore, migration of autoimmune T cells into the brain would be expected to be assisted by over-expression of transcripts encoding for vascular endothelial growth factor (**VEGF**) in lines from MS patients. **VEGF** enhances vascular permeability and may facilitate migration of lymphocytes into the CNS and induction of inflammatory reactions in the brain.

***Downregulated Genes in MS-Derived T-cells*** - The profile of gene expression in MS-derived T-cells (Figure 4, and Table V) indicates a suppression of apoptosis-related functions in the diseased state. One aspect of failure to induce apoptosis in the MS-derived T cell lines is the significant down-regulation of the gene encoding for the pro-apoptotic molecule **TNF**. A reduction in **TNF** could also contribute to a reduction in the ratio of pro- and anti-apoptotic transcript expression in the anti-MOG T cell lines from MS patients compared to healthy controls. Indeed, inadequate apoptosis present in MS autoreactive T cell lines could lead to insufficient deletion of autoimmune activated T cell clones and increase susceptibility to autoimmunity.

In addition, effectors of MHC class I presentation were revealed to be down-regulated in MS patients' cells. Such down-regulated expression includes the transcript for the **proteasome PA28 complex**, known to be a principal provider of MHC class I-presented peptides in antigen presenting cells, and **HSP70 1A and 1B** variants. **TNF** is also known to stimulate MHC class I presentation in addition to induction of apoptosis. The findings presented herein indicate that a weaker antigenic MHC class I presenting capability might distinguish MS-patient derived T cell lines from their healthy counterparts, and providing powerful diagnostic tools. It is conceivable that a lower expression of

MHC class-I on CD4 autoimmune T cells might enable them to escape regulation by CD8 cells that recognize autoimmune idiotypes.

Taken together the combined effects of down-regulation of apoptosis associated genes, up regulation of anti-apoptotic genes, increased expansion capability by autoreactive T cells and enhanced ability to penetrate the CNS may lead to perpetuated pathologic cellular proliferation and tissue destruction within the CNS characteristic of MS, along with increased resistance to regulation. The specific gene expression profiles described herein can define some of the requirements for an individual to develop MS, and thus have important predictive value, especially in determining MS in the “probable” stage. It is noteworthy that despite activation in vitro with the same MOG epitope, anti-MOG T cells from healthy subjects did not attain the gene expression profile that characterized the MS patient-derived cells. The findings support the concept that not all autoimmune T cells are equal; autoimmune T cells from MS patients follow a unique pattern of T cell activation that appears to be more resilient to apoptosis and can support long term survival. Although T cell lines derived from MS patients and healthy donors responded to the same autoantigen, were both activated T cell populations that proliferated extensively in the presence of IL-2, the gene expression imprints that are unique to each group were preserved. These findings indicate the existence of different T-cell activation mechanisms. The nature of the stimuli that generate aberrant autoimmune T-cell gene expression has yet to be identified in order to determine whether their formation is merely the result of the chronic immune stimulation driven by other factors in MS, or whether such T cells function as primary drivers of the MS process. Characterization of such driver T cells, dictating the state of immunity/autoimmunity can also greatly contribute to understanding autoimmunity and possibly also for designing effective treatments for MS.

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**TABLES I-V**

**Table I: Gene Expression Profile from PBMCs of MS vs. Healthy**

Affymetrix ID no:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
40289_at	U78107	8.55E-11	1.94E-11	4.04E-12	-0.43769	NAPG
39402_at	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
41499_at	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
1953_at	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF
189_s_at	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	HSUROKR7
38873_at	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0800
41169_at	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
242_at	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
40385_at	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA20
1983_at	X68452	2.57E-08	2.93E-09	9.12E-11	-0.26618	CCND2
32133_at	AB011161	2.57E-08	2.93E-09	9.64E-11	0.63432	PIP5K1C
37579_at	L47738	2.57E-08	2.93E-09	7.54E-09	0.31646	PIR121
1209_at	U78798	2.57E-08	2.93E-09	1.11E-06	-0.3172	TRAF6
40365_at	M63904	2.57E-08	7.16E-09	5.38E-09	-0.59612	GNA15
35227_at	U72066	2.57E-08	7.16E-09	4.33E-08	-0.34482	RBBP8
37936_at	AI184802	2.64E-07	1.61E-08	2.67E-09	-0.21576	HPRP4P
41831_at	AF077820	2.64E-07	1.61E-08	2.91E-08	0.656852	LRP5
279_at	L13740	2.64E-07	1.61E-08	5.83E-08	-1.45891	NR4A1
39561_at	AL008583	2.64E-07	1.61E-08	1.12E-08	0.250082	
34857_at	Z24724	2.64E-07	1.61E-08	5.96E-09	-1.10426	
34476_r at	D30783	2.57E-08	2.19E-08	8.95E-10	-1.65011	EREG
34405_at	U47927	2.57E-08	2.19E-08	5.53E-09	0.545592	USP5
32021_at	AI560890	2.57E-08	2.19E-08	1.80E-07	0.179028	
37185_at	Y00630	2.57E-08	3.69E-08	6.65E-09	-2.38485	SERPINB2
34210_at	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
36100_at	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
36680_at	M24895	2.11E-06	1.08E-07	1.72E-08	0.476779	AMY2B
33598_r at	AF054176	2.11E-06	1.08E-07	6.47E-09	-0.58138	C1orf7
33943_at	L20941	2.64E-07	1.08E-07	1.78E-06	-0.58618	FTH1
1125_s at	L05424	2.11E-06	1.08E-07	2.27E-09	-0.58081	HUMSCG19
39797_at	AB002347	2.11E-06	1.08E-07	7.19E-10	0.371731	KIAA0349
41431_at	AB023153	2.11E-06	1.08E-07	1.82E-08	0.895842	KIAA0936
40870_g at	AF069517	2.11E-06	1.08E-07	4.91E-07	0.399638	RBM6
32444_at	X69392	2.64E-07	1.08E-07	1.10E-08	0.297444	RPL26
36060_at	U51920	2.11E-06	1.08E-07	7.01E-08	-0.28142	SRP54
1139_at	L22075	2.64E-07	1.71E-07	1.10E-08	-0.55736	GNA13
1520_s at	X04500	2.64E-07	1.71E-07	3.43E-10	-2.12121	IL1B
39417_at	AB028951	2.64E-07	1.71E-07	8.78E-09	0.543028	KIAA1028
35926_s at	AF004230	2.64E-07	1.71E-07	3.06E-07	0.349166	LILRB1
35165_at	AF070582	2.64E-07	1.71E-07	3.23E-08	-0.19773	MGC13033
39183_at	X66363	2.64E-07	1.71E-07	6.53E-07	-0.24505	PCTK1
1603_g at	L33881	2.64E-07	1.71E-07	5.06E-08	-0.59585	PRKCI



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33513 at	U33017	2.64E-07	1.71E-07	5.20E-07	0.373581	SLAM
38988 at	AJ007042	2.64E-07	1.71E-07	2.10E-07	0.170935	WHSC1
39755 at	Z93930	2.64E-07	1.71E-07	2.42E-05	-0.39839	XBP1
37233 at	AF079167	2.64E-07	1.71E-07	7.37E-10	-1.93249	
31472 s at	AF098641	2.64E-07	1.71E-07	1.56E-07	-0.41172	
1181 at	HG3227- HT3404	2.64E-07	1.71E-07	1.68E-08	-0.25361	
38104 at	U78302	2.64E-07	1.71E-07	2.41E-08	0.329878	
34707 at	U91543	2.64E-07	2.49E-07	2.01E-07	0.478678	CHD3
33993 at	M22919	2.64E-07	2.49E-07	9.52E-08	-0.81053	MYL6
41796 at	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
37536 at	Z11697	1.37E-05	4.08E-07	3.55E-06	-1.21033	CD83
32033 at	AL096780	1.37E-05	4.08E-07	2.13E-06	0.34487	CHKL
32539 at	U51205	1.37E-05	4.08E-07	2.65E-07	-0.76279	COP9
35936 g at	Y08683	1.37E-05	4.08E-07	4.71E-06	0.492738	CPT1B
32962 at	S52028	2.11E-06	4.08E-07	9.62E-08	-0.81662	CTH
37365 at	X63368	2.11E-06	4.08E-07	2.30E-08	-0.55432	DNAJB2
37825 at	M84443	1.37E-05	4.08E-07	4.08E-07	0.303567	GALK2
496 s at	U32324	1.37E-05	4.08E-07	3.21E-08	0.334966	IL11RA
41077 at	AB011115	1.37E-05	4.08E-07	3.39E-07	0.382809	KIAA0543
38854 at	AB014535	1.37E-05	4.08E-07	1.04E-06	0.285282	KIAA0635
41485 at	X02152	1.37E-05	4.08E-07	4.63E-08	-0.75601	LDHA
37819 at	AF007130	2.11E-06	4.08E-07	2.51E-06	0.391811	LOC54104
35273 at	AF007151	1.37E-05	4.08E-07	3.25E-06	0.468343	MMS19L
37283 at	X82209	2.11E-06	4.08E-07	1.37E-09	-0.45281	MN1
38064 at	X79882	1.37E-05	4.08E-07	1.78E-07	0.520965	MVP
38276 at	U91616	1.37E-05	4.08E-07	1.27E-07	-0.80419	NFKBIE
38911 at	U41815	1.37E-05	4.08E-07	2.16E-07	-0.96931	NUP98
32784 at	AB011108	1.37E-05	4.08E-07	4.39E-07	0.453498	PRP4
36312 at	L40377	1.37E-05	4.08E-07	3.49E-07	-0.79409	SERPINB8
39159 at	X99656	1.37E-05	4.08E-07	1.68E-06	-0.23553	SH3GL1
40723 at	AJ010059	2.11E-06	4.08E-07	2.95E-06	0.2235	SIT
33803 at	J02973	1.37E-05	4.08E-07	2.93E-07	-1.30804	THBD
32715 at	N90862	1.37E-05	4.08E-07	3.28E-08	0.43576	VAMP8
40729 s at	Y14768	1.37E-05	4.08E-07	7.26E-08	0.248383	
37723 at	U47414	2.11E-06	7.73E-07	2.31E-06	0.370736	CCNG2
32259 at	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1
38429 at	U29344	2.11E-06	7.73E-07	2.35E-07	-0.43842	FASN
35450 s at	AF015553	2.11E-06	7.73E-07	2.61E-07	0.61214	GTF2I
37571 at	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1058
197 at	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
430 at	X00737	2.11E-06	7.73E-07	5.21E-08	-0.67074	NP
36159 s at	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
39691 at	AB007960	2.11E-06	7.73E-07	7.96E-06	0.447772	SH3GLB1
162 at	U44839	2.11E-06	7.73E-07	2.54E-07	-0.97008	USP11
38252 s at	U84007	7.44E-05	1.28E-06	0.000235	0.236422	AGL

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1347 at	S78187	7.44E-05	1.28E-06	1.95E-05	0.203265	CDC25B
38466 at	X82153	7.44E-05	1.28E-06	2.27E-06	0.47844	CTSK
41335 at	AL050084	7.44E-05	1.28E-06	5.26E-05	0.509331	DC8
32716 at	X62535	1.37E-05	1.28E-06	5.68E-07	0.243937	DGKA
38555 at	AB026436	7.44E-05	1.28E-06	0.000219	-0.7589	DUSP10
41425 at	M98833	7.44E-05	1.28E-06	1.52E-06	0.434288	FLI1
33191 at	AW051579	1.37E-05	1.28E-06	7.58E-07	0.593476	FLJ10512
40268 at	X16706	7.44E-05	1.28E-06	1.23E-06	-1.09747	FOSL2
41323 at	U90917	1.37E-05	1.28E-06	3.89E-07	0.433406	FOXMI
34609 g at	M24194	7.44E-05	1.28E-06	4.38E-06	0.560895	GNB2L1
39392 at	AJ002190	7.44E-05	1.28E-06	2.17E-08	0.33775	GNPAT
36614 at	X87949	7.44E-05	1.28E-06	4.05E-07	-0.54468	HSPA5
35303 at	U96876	7.44E-05	1.28E-06	3.54E-06	-0.45317	INSIG1
38349 at	AF038564	1.37E-05	1.28E-06	2.05E-07	-0.40446	ITCH
34034 at	D80011	7.44E-05	1.28E-06	4.20E-07	-0.35073	KIAA0189
35851 g at	AI950382	1.37E-05	1.28E-06	1.63E-07	-0.74128	KIAA0585
36458 at	AB023235	7.44E-05	1.28E-06	1.43E-05	0.311216	KIAA1018
36862 at	AB029038	7.44E-05	1.28E-06	7.62E-05	0.364386	KIAA1115
33456 at	U24166	7.44E-05	1.28E-06	7.52E-06	-0.45293	MAPRE1
40362 at	X61498	7.44E-05	1.28E-06	8.80E-07	-0.49884	NFKB2
190 at	U12767	7.44E-05	1.28E-06	2.84E-07	-1.23483	NR4A3
35741 at	U85245	7.44E-05	1.28E-06	4.57E-07	0.365266	PIP5K2B
38120 at	U50928	7.44E-05	1.28E-06	4.72E-06	0.302213	PKD2
525 g at	U13695	7.44E-05	1.28E-06	1.11E-05	0.805607	PMS1
32213 at	AA203527	1.37E-05	1.28E-06	1.18E-07	0.281992	RPP20
38029 at	J02939	7.44E-05	1.28E-06	2.16E-07	-0.87844	SLC3A2
40885 s at	N30151	7.44E-05	1.28E-06	5.05E-05	0.393521	STX16
34356 at	U52960	2.11E-06	1.28E-06	1.51E-07	-0.84863	SURB7
32756 at	AF030249	1.37E-05	1.28E-06	1.98E-07	0.534547	
40721 g at	AL022398	7.44E-05	1.28E-06	8.09E-08	0.919627	
1877 g at	HG1103- HT1103	1.37E-05	1.28E-06	1.16E-07	-0.39165	
37411 at	D30758	2.11E-06	1.80E-06	1.58E-05	0.27738	CENTB1
31935 s at	U75968	2.11E-06	1.80E-06	4.36E-06	0.139542	DDX11
38326 at	M69199	2.11E-06	1.80E-06	1.45E-07	-1.9021	G0S2
39781 at	U20982	2.11E-06	1.80E-06	1.20E-08	-0.67125	IGFBP4
40498 g at	AF040707	2.11E-06	1.80E-06	3.57E-07	0.289845	NPR2L
32253 at	AB007927	2.11E-06	1.80E-06	2.12E-07	0.323787	RERE
39388 at	AA902713	2.11E-06	1.80E-06	1.44E-06	0.474378	
32105 f at	U66063	2.11E-06	2.24E-06	4.70E-07	0.277185	CAMK2G
41215 s at	D13891	2.11E-06	2.24E-06	4.57E-05	-0.20577	ID2
39976 at	AL050087	2.11E-06	2.24E-06	1.27E-07	-0.31279	KIAA1785
35970 g at	N23137	2.11E-06	2.24E-06	2.06E-07	0.247311	MPHOSPH9
40564 at	N42007	2.11E-06	2.24E-06	9.19E-05	0.167986	NUP50
1231 at	M74525	2.11E-06	2.24E-06	3.50E-07	-0.61792	UBE2B
37794 at	AF035281	2.11E-06	2.24E-06	4.87E-07	0.472445	

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38491 at	U11732	1.37E-05	3.17E-06	3.04E-07	-0.22574	ETV6
34661 at	AB002348	1.37E-05	3.17E-06	2.49E-07	0.576346	KIAA0350
40431 at	AB007891	1.37E-05	3.17E-06	3.99E-05	0.196376	KIAA0431
39257 at	AI754391	1.37E-05	3.17E-06	1.72E-06	-0.27657	KLF12
35234 at	D50406	1.37E-05	3.17E-06	2.65E-05	0.461907	RECK
35142 at	AF070617	1.37E-05	3.17E-06	3.23E-07	0.323494	
39791 at	M23114	2.11E-06	4.08E-06	1.59E-07	-0.96141	ATP2A2
1445 at	AF014958	2.11E-06	4.08E-06	1.05E-07	-0.42152	CCRL2
36639 at	AF067853	1.37E-05	4.31E-06	5.02E-06	0.361707	ADSL
1252 at	M73547	1.37E-05	4.31E-06	9.20E-08	0.438897	D5S346
39296 at	W28319	1.37E-05	4.31E-06	1.50E-05	0.294631	FBLN1
39650 s at	AB007895	1.37E-05	4.31E-06	9.61E-07	0.186643	KIAA0435
35317 at	AB014579	1.37E-05	4.31E-06	6.08E-08	0.367966	MGEA5
31675 s at	AF019083	1.37E-05	4.31E-06	8.34E-07	0.17011	PTENP1
38859 at	AL080141	1.37E-05	4.31E-06	2.42E-07	0.330868	SEC31B-1
33810 at	AF110377	1.37E-05	4.31E-06	3.05E-05	0.361232	TRRAP
36260 at	AB002448	1.37E-05	4.31E-06	2.45E-07	0.468926	
34239 at	AL049787	1.37E-05	4.31E-06	7.11E-06	0.311278	
1527 s at	U50527	1.37E-05	4.31E-06	5.11E-06	0.416543	
33588 at	Z32860	1.37E-05	4.31E-06	7.81E-06	0.133192	
39562 at	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP1
493 at	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1D
38296 at	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP586D2223
1788 s at	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
37938 at	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15552
280 g at	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1
36079 at	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
38518 at	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
34779 at	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GALNACIV
33328 at	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
40881 at	X64330	7.44E-05	6.03E-06	2.27E-06	0.297851	ACLY
37229 at	U49844	7.44E-05	6.03E-06	3.67E-07	0.47168	ATR
37760 at	AB015019	7.44E-05	6.03E-06	2.75E-07	-0.24515	BAIAP2
39231 at	AF006513	0.000344	6.03E-06	4.48E-05	-1.45973	CHD1
806 at	U56998	0.000344	6.03E-06	3.70E-06	-0.74294	CNK
32066 g at	S68134	0.000344	6.03E-06	8.37E-07	-1.64652	CREM
32065 at	S68134	0.000344	6.03E-06	4.35E-06	-2.47105	CREM
32067 at	S68271	0.000344	6.03E-06	3.03E-06	-2.07185	CREM
38974 at	AF021819	0.000344	6.03E-06	4.41E-05	0.298771	DJ-1
38628 at	AF029777	1.37E-05	6.03E-06	8.27E-07	0.290159	GCN5L2
37706 at	U28811	0.000344	6.03E-06	1.33E-06	0.32855	GLG1
1237 at	S81914	0.000344	6.03E-06	4.18E-07	-1.59146	IER3
35116 at	X80821	0.000344	6.03E-06	8.51E-05	-0.5606	KIAA0874
1774 at	L06895	7.44E-05	6.03E-06	1.12E-05	-0.1928	MAD
40661 at	D78579	1.37E-05	6.03E-06	4.25E-07	-1.65638	NR4A3

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40662 g at	D78579	7.44E-05	6.03E-06	9.62E-07	-1.61438	NR4A3
40659 at	U12767	0.000344	6.03E-06	2.55E-07	-2.13744	NR4A3
210 at	M95678	0.000344	6.03E-06	2.00E-06	0.432923	PLCB2
31860 at	X51804	0.000344	6.03E-06	7.23E-05	-0.19283	PMI
36856 at	W28743	0.000344	6.03E-06	2.78E-06	-0.28926	PP1628
32227 at	X17042	7.44E-05	6.03E-06	6.64E-06	-0.36481	PRG1
32186 at	M80244	0.000344	6.03E-06	2.72E-06	-0.8522	SLC7A5
31888 s at	AF001294	1.37E-05	6.03E-06	1.23E-06	-0.76359	TSSC3
38523 f at	D49677	7.44E-05	6.03E-06	4.18E-06	0.198707	U2AF1RS2
41242 at	AB011004	0.000344	6.03E-06	1.41E-06	-1.34073	UAP1
41430 at	AB011113	1.37E-05	6.03E-06	3.74E-07	0.444795	WDR7
41488 at	AC002394	0.000344	6.03E-06	0.001473	0.17105	
34333 at	AL021707	0.000344	6.03E-06	4.95E-06	-2.21462	
40720 at	AL022398	7.44E-05	6.03E-06	1.10E-07	0.79713	
40349 at	AL049442	0.000344	6.03E-06	8.09E-06	0.621935	
36929 at	U17760	0.000344	6.03E-06	4.25E-06	-0.84472	
32372 at	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
36133 at	AL031058	1.37E-05	8.66E-06	0.000375	0.149046	DSP
41406 at	AL080172	1.37E-05	8.66E-06	1.89E-05	0.098968	FLJ21919
34022 at	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
39823 at	U06631	1.37E-05	8.66E-06	1.31E-05	0.486332	H326
37497 at	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
41266 at	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
35039 at	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0276
39551 at	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1696
32329 at	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTHB6
38160 at	AF011333	1.37E-05	8.66E-06	1.55E-05	0.342503	LY75
40138 at	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34-34KD
33849 at	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
40137 at	M31724	1.37E-05	8.66E-06	0.000172	-0.2601	PTPN1
32579 at	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMARCA4
36894 at	AL031846	1.37E-05	8.66E-06	0.000418	0.38404	
39093 s at	Y12059	7.44E-05	1.51E-05	5.64E-06	-0.46008	BRD4
32977 at	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
424 s at	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
32181 at	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2
36021 at	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
35434 at	L16794	7.44E-05	1.51E-05	2.23E-05	-0.27553	MEF2D
1652 at	U77735	7.44E-05	1.51E-05	5.66E-06	0.574142	PIM2
39734 at	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
31410 at	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
31508 at	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
34962 at	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	
642 s at	L76528	7.44E-05	1.51E-05	6.14E-06	-0.39652	
39749 at	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	
32567 at	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK

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40607 at	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL2
554 at	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
39037 at	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
1373 at	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
37189 at	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	
32130 at	W25984	7.44E-05	2.35E-05	1.42E-05	0.482493	ACTA1
36586 at	U78521	0.000344	2.35E-05	2.53E-05	0.320909	AIP
34898 at	M30704	0.000344	2.35E-05	1.65E-05	-0.37795	AREG
35765 at	X91504	0.001377	2.35E-05	0.00016	0.233217	ARFRP1
32563 at	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B3
38201 at	U21551	0.001377	2.35E-05	7.60E-05	-0.3088	BCAT1
40790 at	AB004066	0.000344	2.35E-05	6.57E-05	-0.60905	BHLHB2
2036 s at	M59040	0.001377	2.35E-05	2.82E-06	-0.46271	CD44
40619 at	M91670	0.001377	2.35E-05	0.001649	-0.47538	E2-EPF
38868 at	U43774	0.000344	2.35E-05	8.80E-07	-0.39938	FCAR
41177 at	AW024285	0.000344	2.35E-05	6.99E-06	-0.42098	FLJ12443
40615 at	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
36484 at	AI935146	0.000344	2.35E-05	2.05E-06	-0.46726	GALNT3
35289 at	AJ011679	0.001377	2.35E-05	4.67E-05	0.243248	GAPCENA
34724 at	AI670100	7.44E-05	2.35E-05	7.70E-07	0.22677	GRLF1
40113 at	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
31977 at	M92432	0.000344	2.35E-05	4.31E-05	0.363033	GUCY2D
38771 at	D50405	0.001377	2.35E-05	0.000688	0.387926	HDAC1
1636 g at	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	HSABLGR3
37679 at	Y10313	0.001377	2.35E-05	0.003201	-0.35345	IFRD1
33281 at	D63485	0.000344	2.35E-05	9.04E-05	0.31177	IKKE
41524 at	L08488	0.000344	2.35E-05	7.54E-06	-0.37883	INPP1
39753 at	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5
37619 at	D42084	0.001377	2.35E-05	7.39E-06	0.222195	KIAA0094
39783 at	D43947	7.44E-05	2.35E-05	0.000104	0.269941	KIAA0100
40018 at	AB007870	0.000344	2.35E-05	0.000108	-0.64362	KIAA0410
35850 at	AI950382	0.000344	2.35E-05	0.000122	-0.65985	KIAA0585
34353 at	AB014548	7.44E-05	2.35E-05	2.77E-05	0.431229	KIAA0648
31909 at	AB018297	0.001377	2.35E-05	0.000836	0.195704	KIAA0754
34751 at	AI970189	0.000344	2.35E-05	6.16E-07	-0.75934	KIAA0997
39057 at	L04733	0.001377	2.35E-05	8.84E-07	0.306455	KNS2
1857 at	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH7
36126 at	U18919	7.44E-05	2.35E-05	1.05E-05	0.271231	NBP
40823 s at	U85430	0.001377	2.35E-05	0.000315	0.317554	NFATC3
544 at	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
36968 s at	AL050353	0.000344	2.35E-05	4.42E-06	0.179352	OIP2
33705 at	L20971	0.001377	2.35E-05	0.00089	-0.49725	PDE4B
41281 s at	AF060502	7.44E-05	2.35E-05	0.000114	-0.18239	PEX10
36480 at	X80497	0.001377	2.35E-05	0.000245	0.313262	PHKA2
38090 at	AL050371	0.000344	2.35E-05	3.70E-06	0.493288	PISD
33543 s at	U77718	7.44E-05	2.35E-05	6.60E-06	0.352996	PNN

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39747 at	U52427	0.001377	2.35E-05	0.000282	0.329478	POLR2G
34914 at	U94778	0.000344	2.35E-05	1.18E-05	0.282929	PSTPIP1
843 at	U48296	0.001377	2.35E-05	0.00011	-0.89871	PTP4A1
1491 at	M31166	0.001377	2.35E-05	0.000256	-0.38484	PTX3
35152 at	AJ001016	7.44E-05	2.35E-05	1.08E-05	-0.28245	RAMP3
39847 at	AF040965	0.001377	2.35E-05	0.001101	-0.38591	RES4-25
36674 at	J04130	0.000344	2.35E-05	3.02E-06	-0.62071	SCYA4
33143 s at	U81800	0.000344	2.35E-05	4.28E-05	-0.49523	SLC16A3
41592 at	AB000734	0.001377	2.35E-05	0.000883	-0.58764	SSI-1
39779 at	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP1
38473 at	M63180	0.001377	2.35E-05	1.03E-05	-0.33301	TARS
33439 at	D15050	0.001377	2.35E-05	0.000192	-1.12874	TCF8
1106 s at	M12959	7.44E-05	2.35E-05	1.61E-06	0.128482	TRA@
429 f at	X00734	0.001377	2.35E-05	0.000384	-0.34516	TUBB5
31882 at	AJ001340	0.001377	2.35E-05	4.21E-05	0.181208	U3-55K
37729 at	Y08614	0.001377	2.35E-05	6.92E-05	0.305659	XPO1
37842 at	AF054589	0.000344	2.35E-05	1.98E-06	0.945394	
33734 at	AL022398	7.44E-05	2.35E-05	2.40E-06	0.493166	
38990 at	AL031178	7.44E-05	2.35E-05	3.18E-05	0.410068	
33687 at	AL049782	7.44E-05	2.35E-05	7.66E-07	0.237794	
1171 s at	HG1471- HT3923	0.001377	2.35E-05	0.000519	0.203133	
706 at	HG4582- HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
32061 at	U96629	0.001377	2.35E-05	1.00E-04	0.277256	
37218 at	D64110	7.44E-05	2.58E-05	7.49E-05	-0.51036	BTG3
32583 at	J04111	7.44E-05	2.58E-05	0.000108	-1.60276	JUN
1895 at	J04111	7.44E-05	2.58E-05	4.68E-05	-1.14014	JUN
41483 s at	X56681	7.44E-05	2.58E-05	0.000112	-0.48711	JUND
38031 at	D21853	7.44E-05	2.58E-05	0.000403	-0.25594	KIAA0111
36926 at	X80692	7.44E-05	2.58E-05	3.44E-05	-1.1939	MAPK6
545 g at	S76638	7.44E-05	2.58E-05	5.23E-05	-0.46026	NFKB2
33863 at	U65785	7.44E-05	2.58E-05	9.67E-06	-0.2389	ORP150
33421 s at	AB016247	7.44E-05	2.58E-05	3.13E-05	-0.57287	SC5DL
38404 at	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2
553 g at	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHGAP1
33908 at	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
1499 at	L10413	1.37E-05	2.81E-05	6.46E-06	0.207231	FNTA
39733 at	AF055001	1.37E-05	2.81E-05	9.78E-06	-0.9457	HERPUD1
41502 at	AI523538	1.37E-05	2.81E-05	0.004471	-0.1584	HIPK3
414 at	X59373	1.37E-05	2.81E-05	1.31E-05	-0.22992	HOXD10
39348 at	X99209	1.37E-05	2.81E-05	2.65E-05	0.239777	HRMT1L1
202 at	M65217	1.37E-05	2.81E-05	1.02E-05	0.33377	HSF2
36985 at	X17025	1.37E-05	2.81E-05	1.45E-05	-0.44351	IDI1
37319 at	M35878	1.37E-05	2.81E-05	4.29E-05	-0.25267	IGFBP3
41728 at	D63486	1.37E-05	2.81E-05	9.69E-06	0.235319	KIAA0152
37914 at	AB002303	1.37E-05	2.81E-05	1.86E-05	-0.39642	KIAA0305

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535 s at	U20816	1.37E-05	2.81E-05	4.92E-05	-0.20145	NFKB2
1269 at	M61906	1.37E-05	2.81E-05	5.93E-06	-0.39875	PIK3R1
524 at	U13695	1.37E-05	2.81E-05	1.31E-05	0.362255	PMS1
35859 f at	U38979	1.37E-05	2.81E-05	3.95E-05	0.158105	PMS2L9
382 at	X70218	1.37E-05	2.81E-05	2.44E-06	-0.74691	PPP4C
39975 at	AC002400	1.37E-05	2.81E-05	2.28E-06	-0.25834	
36336 s at	AC005390	1.37E-05	2.81E-05	2.99E-05	-0.24231	
34188 at	AF070606	1.37E-05	2.81E-05	1.48E-06	-0.89337	
1842 at	HG2724- HT2820	1.37E-05	2.81E-05	5.17E-06	-1.33814	
33334 at	X84194	7.44E-05	4.67E-05	6.38E-05	0.23578	ACYPI
32607 at	AF039656	0.00482	4.67E-05	0.000251	-0.73273	BASP1
37112 at	AB002384	0.00482	4.67E-05	4.22E-05	0.548091	C6orf32
33774 at	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
486 at	U60521	7.44E-05	4.67E-05	8.13E-06	-0.36762	CASP9
1924 at	U11791	0.00482	4.67E-05	0.000363	-1.0232	CCNH
35695 at	U67615	0.00482	4.67E-05	0.000948	1.23433	CHS1
41413 at	AF037339	0.000344	4.67E-05	1.59E-05	-0.33549	CLPTM1
1789 at	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COP55
41309 g at	U37408	7.44E-05	4.67E-05	3.06E-05	0.157458	CTBP1
37127 at	AB023143	0.00482	4.67E-05	0.001982	0.215415	DEFCAP
41233 at	AB014888	0.001377	4.67E-05	0.000204	-0.34841	DNAJB6
38037 at	M60278	0.00482	4.67E-05	3.33E-05	-0.9007	DTR
40606 at	U88629	0.000344	4.67E-05	9.58E-07	-0.32607	ELL2
1885 at	M31899	0.000344	4.67E-05	0.000339	0.274507	ERCC3
39799 at	M94856	7.44E-05	4.67E-05	4.99E-06	-0.23847	FABP5
36183 at	X86779	0.001377	4.67E-05	1.08E-05	0.140032	FASTK
1772 s at	L00634	0.00482	4.67E-05	0.00019	0.205256	FNTA
39822 s at	AF078077	0.000344	4.67E-05	1.44E-05	-1.47649	GADD45B
717 at	D87119	7.44E-05	4.67E-05	4.62E-06	0.557116	GS3955
33932 at	X17644	7.44E-05	4.67E-05	6.72E-06	-0.71963	GSPT1
37393 at	L19314	0.00482	4.67E-05	0.000922	-0.35113	HRY
1796 s at	U05681	7.44E-05	4.67E-05	3.37E-06	-0.35383	HSBCL3S2
1610 s at	J00139	0.00482	4.67E-05	0.000196	-0.12797	HUMFOL5
32640 at	M24283	0.000344	4.67E-05	3.71E-06	-1.32611	ICAM1
1737 s at	M62403	7.44E-05	4.67E-05	5.57E-07	-0.53749	IGFBP4
1369 s at	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
371 at	Z56281	0.001377	4.67E-05	0.000243	0.309173	IRF3
2061 at	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
32272 at	K00558	0.001377	4.67E-05	0.002498	0.12909	K-ALPHA-1
34843 at	AL044599	0.001377	4.67E-05	8.81E-05	0.321294	KIAA0222
41387 r at	AB002344	0.000344	4.67E-05	1.04E-05	-0.39307	KIAA0346
37363 at	AB007889	7.44E-05	4.67E-05	2.33E-05	0.255643	KIAA0429
41243 at	AB007916	0.00482	4.67E-05	0.000147	0.493018	KIAA0447
37375 at	AB014538	0.000344	4.67E-05	1.98E-06	-0.63923	KIAA0638
34831 at	AF055004	7.44E-05	4.67E-05	9.29E-05	0.200537	KIAA0763

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40670 at	A1148772	0.000344	4.67E-05	4.18E-06	-1.02619	KYNU
35160 at	AF064491	0.00482	4.67E-05	0.000148	-0.54215	LDB1
1846 at	L78132	7.44E-05	4.67E-05	5.15E-07	0.358576	LGALS8
963 at	X83441	7.44E-05	4.67E-05	6.75E-06	-0.17796	LIG4
39428 at	AF055581	7.44E-05	4.67E-05	5.69E-06	-1.05728	LNK
40456 at	AL049963	0.000344	4.67E-05	8.36E-07	-0.74421	LOC64116
32246 g at	AF014837	0.00482	4.67E-05	0.000636	0.325349	M6A
1891 at	D14497	0.001377	4.67E-05	3.68E-05	-0.58619	MAP3K8
1439 s at	X75346	7.44E-05	4.67E-05	1.99E-05	-0.37877	MAPKAPK2
38278 at	M62324	0.001377	4.67E-05	5.46E-05	-0.44552	MRF-1
41220 at	AB023208	0.000344	4.67E-05	1.37E-05	0.293901	MSF
38035 at	AF072928	0.001377	4.67E-05	1.13E-05	-0.3089	MTMR6
38692 at	AF045451	0.000344	4.67E-05	6.34E-06	-0.40149	NAB1
1378 g at	M58603	7.44E-05	4.67E-05	1.28E-06	-0.73537	NFKB1
519 g at	U07132	0.00482	4.67E-05	0.001821	-0.14679	NR1H2
37623 at	X75918	7.44E-05	4.67E-05	3.50E-05	-1.61126	NR4A2
547 s at	S77154	0.00482	4.67E-05	0.000304	-1.33785	NR4A2
33752 at	AB020657	0.00482	4.67E-05	2.75E-05	-0.50544	NS1-BP
1959 at	D88674	7.44E-05	4.67E-05	6.26E-06	-0.99818	OAZIN
39943 at	U27459	0.00482	4.67E-05	3.39E-05	0.430016	ORC2L
358 at	AF000545	7.44E-05	4.67E-05	3.48E-06	-0.85393	P2Y10
38270 at	AF005043	7.44E-05	4.67E-05	2.70E-06	0.408592	PARG
38365 at	AF026086	0.000344	4.67E-05	2.66E-06	0.297942	PEX1
36864 at	AJ001625	7.44E-05	4.67E-05	9.91E-05	0.36837	PEX3
36963 at	U30255	0.001377	4.67E-05	0.000826	0.325906	PGD
35373 at	M61906	0.000344	4.67E-05	0.000611	-0.2492	PIK3R1
33181 at	M60483	0.000344	4.67E-05	3.17E-05	-0.32565	PPP2CA
1241 at	U14603	7.44E-05	4.67E-05	4.46E-05	0.427268	PTP4A2
40869 at	AF069517	0.001377	4.67E-05	0.000441	0.330897	RBM6
570 at	M83221	0.000344	4.67E-05	1.58E-05	-0.26782	RELB
38290 at	AF037195	0.00482	4.67E-05	8.27E-05	0.959619	RGS14
1127 at	L07597	0.00482	4.67E-05	0.000169	0.277243	RPS6KA1
1866 g at	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
36979 at	M20681	0.001377	4.67E-05	1.92E-05	-0.99917	SLC2A3
36542 at	AF030409	7.44E-05	4.67E-05	7.66E-06	0.412043	SLC9A6
37410 at	AJ224358	0.00482	4.67E-05	0.009613	0.14432	SURF5
35634 at	U49928	0.000344	4.67E-05	6.31E-06	0.352648	TAB1
38805 at	X89750	7.44E-05	4.67E-05	7.38E-06	-1.51687	TGIF
32831 at	AA453183	0.001377	4.67E-05	4.48E-05	-0.61646	TIM17
1372 at	M31165	7.44E-05	4.67E-05	1.38E-06	-0.34617	TNFAIP6
31742 at	AF064090	0.001377	4.67E-05	4.05E-05	-0.38921	TNFSF14
39430 at	AF082557	0.001377	4.67E-05	2.23E-06	0.226994	TNKS
38834 at	D87448	0.00482	4.67E-05	0.000735	0.468196	TOPBP1
33866 at	X05276	0.00482	4.67E-05	8.97E-05	-0.50457	TPM4
33253 at	D50919	0.00482	4.67E-05	4.02E-05	0.332326	TRIM14
1410 at	J03258	0.00482	4.67E-05	8.78E-05	-0.33021	VDR



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32388 at	AB007973	0.00482	4.67E-05	0.000146	0.271053	
40878 f at	AF041081	0.00482	4.67E-05	5.92E-05	0.26539	
36250 at	AI889718	7.44E-05	4.67E-05	0.000143	-0.15002	
37043 at	AL021154	0.000344	4.67E-05	2.19E-06	-0.82935	
40711 at	AL049340	0.000344	4.67E-05	4.87E-05	-0.91769	
39324 at	AL050078	0.000344	4.67E-05	1.63E-05	-0.2875	
37442 at	AL050378	0.000344	4.67E-05	5.72E-06	0.360577	
33683 at	D50525	0.000344	4.67E-05	3.02E-06	0.486698	
31697 s at	J04755	7.44E-05	4.67E-05	6.75E-05	-0.37296	
40842 at	M60784	7.44E-05	4.67E-05	1.24E-06	0.559903	
36101 s at	M63978	0.000344	4.67E-05	1.77E-06	-0.44762	
38093 at	U90909	0.00482	4.67E-05	3.74E-05	-0.64272	
31526 f at	X63547	0.001377	4.67E-05	0.000303	0.505712	
32606 at	AA135683	0.000344	5.23E-05	0.000289	-0.69258	BASP1
36209 at	S78771	0.000344	5.23E-05	2.55E-06	-0.31389	BRD2
39411 at	AL080156	0.000344	5.23E-05	3.52E-05	-0.94419	DKFZP434J214
1616 at	D14838	0.000344	5.23E-05	7.34E-06	-0.50648	FGF9
35785 at	W28281	0.000344	5.23E-05	8.96E-06	-1.09149	GABARAPL1
41386 i at	AB002344	7.44E-05	5.23E-05	8.48E-07	-1.00068	KIAA0346
37678 at	U23070	0.000344	5.23E-05	3.62E-05	-0.12321	NMA
1069 at	U04636	0.000344	5.23E-05	2.81E-06	-1.85123	PTGS2
471 f at	U47634	0.000344	5.23E-05	0.002405	-0.21686	TUBB4
1464 at	S73149	0.000344	5.23E-05	0.003714	-0.15741	
36190 at	M63256	0.000344	5.92E-05	6.54E-07	0.454561	CDR2
38003 s at	U94905	0.000344	5.92E-05	2.08E-05	0.388608	DGKZ
40843 at	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP-1A
1479 g at	L10717	0.000344	5.92E-05	0.000158	0.345558	ITK
38149 at	D29642	0.000344	5.92E-05	8.30E-06	0.327019	KIAA0053
36279 at	AB011128	0.000344	5.92E-05	0.000584	0.151161	KIAA0556
39777 at	AF075587	0.000344	5.92E-05	7.55E-06	0.4405	KIAA0916
138 at	U66464	0.000344	5.92E-05	2.93E-05	0.255675	MAP4K1
36127 g at	U18919	0.000344	5.92E-05	0.000573	0.277847	NBP
1980 s at	X58965	0.000344	5.92E-05	7.34E-05	0.231912	NME2
40896 at	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F1
32075 at	D89859	0.000344	5.92E-05	1.56E-05	0.375402	ZFP161
36818 at	AF052100	0.000344	5.92E-05	1.37E-05	0.290021	
39693 at	N53547	7.44E-05	7.24E-05	1.80E-07	0.296678	MGC5508
33909 at	L35013	0.000344	7.24E-05	0.000112	-0.17331	SF3B4
41010 at	Y17829	7.44E-05	7.24E-05	5.49E-06	-0.6508	SYN47
40552 s at	AL049987	7.44E-05	7.24E-05	2.39E-05	0.193082	
37904 s at	X66436	0.000344	7.24E-05	1.88E-06	-0.26662	
39408 at	Z80345	7.44E-05	9.64E-05	7.31E-06	0.412137	ACADS
2002 s at	U27467	7.44E-05	9.64E-05	5.65E-06	-0.56637	BCL2A1
34484 at	AI961669	7.44E-05	9.64E-05	0.000107	-0.1656	BIG2
37294 at	X61123	7.44E-05	9.64E-05	4.17E-07	-1.15256	BTG1
32978 g at	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32

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36650 at	D13639	7.44E-05	9.64E-05	8.56E-06	-0.64255	CCND2
34845 at	AL035398	7.44E-05	9.64E-05	0.000153	0.353395	CGI-51
529 at	U15932	7.44E-05	9.64E-05	0.00031	-1.26603	DUSP5
38599 s at	AD001530	7.44E-05	9.64E-05	3.06E-05	-0.37019	DXS9928E
37762 at	Y07909	7.44E-05	9.64E-05	0.000161	-0.23489	EMP1
38226 at	W27152	7.44E-05	9.64E-05	0.000502	0.186359	FLJ10569
39704 s at	L17131	7.44E-05	9.64E-05	1.48E-05	-0.24039	HMG1Y
38299 at	X04430	7.44E-05	9.64E-05	4.15E-05	-0.21816	IL6
41614 at	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0708
40060 r at	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
35838 at	U90919	7.44E-05	9.64E-05	7.23E-06	-0.50014	LOC57862
40390 at	J05037	7.44E-05	9.64E-05	0.000185	-0.19243	SDS
40638 at	X70944	7.44E-05	9.64E-05	2.08E-05	-0.72892	SFPQ
32165 at	L41887	7.44E-05	9.64E-05	6.74E-06	-0.52203	SFRS7
32649 at	X59871	7.44E-05	9.64E-05	1.91E-05	0.376648	TCF7
38801 at	A1742846	7.44E-05	9.64E-05	0.000374	-0.48069	VAPA
1743 s at	HG2007- HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
32145 at	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	
34979 at	AB018323	7.44E-05	0.000106	2.41E-05	0.432301	GASC1
33916 at	AB023192	7.44E-05	0.000106	0.000138	0.196185	I-1
41372 at	AB020638	7.44E-05	0.000106	5.26E-05	0.233629	KIAA0831
40396 at	U49395	7.44E-05	0.000106	0.001916	0.169175	P2RX5
36935 at	M23379	7.44E-05	0.000106	3.22E-05	0.42571	RASA1
32218 at	AF034176	7.44E-05	0.000106	0.000333	0.332105	
34677 f at	AJ012755	7.44E-05	0.000106	0.000296	0.26445	
38704 at	AB007934	7.44E-05	0.000119	6.08E-06	0.345799	ACF7
37027 at	M80899	7.44E-05	0.000119	2.48E-05	0.419409	AHNAK
34657 at	AB014529	7.44E-05	0.000119	1.84E-05	0.43403	AKAP11
36578 at	U37547	7.44E-05	0.000119	6.74E-06	-0.71736	BIRC2
36634 at	U72649	7.44E-05	0.000119	0.000207	-0.30079	BTG2
34338 at	D49738	7.44E-05	0.000119	0.000136	0.292742	CKAP1
37453 at	AJ006267	7.44E-05	0.000119	7.19E-06	0.427023	CLPX
34404 at	W28167	7.44E-05	0.000119	1.16E-05	0.214921	COPS7A
1243 at	U18300	7.44E-05	0.000119	2.43E-06	0.183171	DDB2
35682 at	A1133727	7.44E-05	0.000119	1.43E-06	0.181464	FLB6421
36647 at	AA526812	7.44E-05	0.000119	0.000106	0.259476	FLJ10326
318 at	D64142	7.44E-05	0.000119	1.66E-05	0.528036	H1FX
38913 at	U60319	7.44E-05	0.000119	0.001064	0.194324	HFE
35372 r at	M17017	7.44E-05	0.000119	1.43E-06	-1.74073	IL8
34336 at	D32053	7.44E-05	0.000119	0.003279	0.222661	KARS
35374 at	AB007914	7.44E-05	0.000119	7.13E-05	0.302838	KIAA0445
35974 at	U10485	7.44E-05	0.000119	7.40E-06	0.270352	LRMP
198 g at	U29656	7.44E-05	0.000119	4.31E-06	0.471876	NME3
33755 at	AB014604	7.44E-05	0.000119	1.72E-05	0.425787	OSBPL3
835 at	U41745	7.44E-05	0.000119	0.00204	0.230274	PDAP1

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858 at	S90469	7.44E-05	0.000119	5.56E-06	-0.2636	POR
875 g at	M26683	7.44E-05	0.000119	3.70E-06	-0.16179	SCYA2
37379 at	X81789	7.44E-05	0.000119	2.23E-05	0.143079	SF3A3
41127 at	L14595	7.44E-05	0.000119	3.55E-05	-0.1953	SLC1A4
38341 at	AL079286	7.44E-05	0.000119	0.000245	0.165851	STAU2
37348 s at	AA845349	7.44E-05	0.000119	7.78E-07	0.457176	TRIP7
40414 at	X59303	7.44E-05	0.000119	0.000124	0.224891	VAR52
41366 at	AB023219	7.44E-05	0.000119	1.41E-05	0.316475	
38438 at	M58603	7.44E-05	0.000129	9.08E-06	-0.56835	NFKB1
32741 at	X77723	7.44E-05	0.000129	0.006788	-0.24317	RAB5EP
41384 at	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
34357 g at	U52960	7.44E-05	0.000129	0.001042	-0.24648	SURB7
38253 at	U84011	0.00482	0.000149	0.000134	0.286331	AGL
32629 f at	U90552	0.000344	0.000149	0.000182	0.288509	BTN3A1
40738 at	M16336	0.00482	0.000149	0.000224	0.218007	CD2
2031 s at	U03106	0.000344	0.000149	0.000252	-0.87784	CDKN1A
38664 at	AB009285	0.001377	0.000149	0.000137	0.235726	CFDP1
34683 at	U63289	0.001377	0.000149	0.001722	-0.43517	CUGBP1
357 at	AF000430	0.00482	0.000149	0.000694	-0.19887	DNMIL
1292 at	L11329	0.001377	0.000149	0.000142	-0.56584	DUSP2
38283 at	AB007619	0.00482	0.000149	0.002073	0.198391	EBAG9
37318 at	X81625	0.00482	0.000149	6.92E-05	-0.80689	ETF1
38318 at	AL050128	0.000344	0.000149	1.81E-05	0.459416	FAM8A1
36669 at	L49169	0.001377	0.000149	8.18E-05	-2.09549	FOSB
37903 at	L25665	0.000344	0.000149	3.34E-06	-0.4513	GNL1
32591 at	AI494623	0.00482	0.000149	0.000304	0.187206	HCDI
40576 f at	D89678	0.001377	0.000149	3.03E-05	0.197298	HNRPD
1635 at	U07563	0.000344	0.000149	1.02E-05	-0.23627	HSABLGR3
40913 at	W28589	0.00482	0.000149	0.000129	0.170457	HSPD1
41258 at	N29665	0.000344	0.000149	3.34E-05	0.593294	KIAA0618
41447 at	AB023207	0.000344	0.000149	8.64E-06	-0.4056	KIAA0990
41710 at	AL079277	0.00482	0.000149	0.000161	0.200656	LOC54103
34770 at	Z14138	0.001377	0.000149	0.000197	-0.85008	MAP3K8
35969 at	N23137	0.001377	0.000149	4.12E-06	0.244083	MPHOSPH9
32738 at	AF050640	0.001377	0.000149	6.03E-05	0.324021	NDUFS2
39735 at	AF069987	0.001377	0.000149	4.44E-05	0.203382	NIT1
41656 at	AF043325	0.000344	0.000149	1.06E-05	0.328186	NMT2
1102 s at	M10901	0.001377	0.000149	1.91E-05	-0.58982	NR3C1
36636 at	M12267	0.000344	0.000149	4.07E-06	-0.3279	OAT
38526 at	U02882	0.00482	0.000149	0.000223	-0.99878	PDE4D
34998 at	AF059531	0.000344	0.000149	6.73E-06	0.546441	PRMT3
39253 s at	M29893	0.001377	0.000149	9.96E-05	-0.15688	RALA
33457 at	AB029028	0.001377	0.000149	9.11E-06	0.482258	RAP140
40391 at	AB007448	0.00482	0.000149	0.000777	-0.319	SLC22A4
37895 at	D87969	0.00482	0.000149	0.001578	0.401991	SLC35A1
40810 at	U66615	0.00482	0.000149	0.000196	0.235993	SMARCC1

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41659 at	U46691	0.00482	0.000149	1.48E-05	-0.85179	SUPT6H
40841 at	AF049910	0.00482	0.000149	0.000373	-0.32787	TACC1
115 at	X14787	0.001377	0.000149	2.88E-05	-0.19161	THBS1
40145 at	AI375913	0.00482	0.000149	0.000905	-0.12102	TOP2A
33679 f at	X02344	0.001377	0.000149	0.00414	-0.20405	TUBB2
37667 at	AF104421	0.000344	0.000149	6.50E-06	0.349373	UROD
1388 g at	J03258	0.000344	0.000149	1.21E-06	-0.58295	VDR
40569 at	M58297	0.000344	0.000149	1.57E-05	0.185829	ZNF42
33215 g at	Y11681	0.000344	0.000149	1.92E-05	0.234481	
41428 at	AF104942	0.001377	0.00019	4.83E-05	0.464438	ABCC5
32146 s at	L07261	0.000344	0.00019	0.003564	0.29763	ADD1
287 at	L19871	0.001377	0.00019	0.000105	-0.19867	ATF3
37661 at	J04027	0.000344	0.00019	0.000133	-0.42466	ATP2B1
41089 at	M83363	0.001377	0.00019	0.004471	0.177565	ATP2B4
31842 at	AF038195	0.000344	0.00019	0.000134	0.281425	BCS1L
36210 g at	S78771	0.001377	0.00019	0.000145	-0.24109	BRD2
650 s at	L07044	0.001377	0.00019	0.000284	0.186013	CAMK2G
1116 at	M28170	0.000344	0.00019	2.96E-05	0.356602	CD19
35228 at	Y08682	0.000344	0.00019	0.000118	0.17398	CPT1B
37509 at	AF046059	0.001377	0.00019	0.000665	0.204072	CREME9
649 s at	L06797	0.001377	0.00019	0.000455	-0.93505	CXCR4
631 g at	L39874	0.000344	0.00019	0.000354	0.353702	DCTD
31839 at	AC004475	0.000344	0.00019	2.86E-05	0.25205	DKFZP434E2216
38265 at	AI538172	0.001377	0.00019	0.000621	0.243057	DKFZp761B2423
37361 at	AF010187	0.000344	0.00019	1.00E-05	0.361895	FIBP
33192 g at	AW051579	0.000344	0.00019	0.000258	0.390285	FLJ10512
40764 at	M22632	0.001377	0.00019	1.34E-05	0.157239	GOT2
413 at	X59372	0.001377	0.00019	0.000528	-0.12959	HOXD9
41088 at	X12433	0.000344	0.00019	1.07E-05	-0.39946	HS1-2
32316 s at	X15183	0.000344	0.00019	0.000645	-0.22973	HSPCA
39353 at	AI912041	0.001377	0.00019	5.21E-05	-0.38517	HSPE1
38661 at	X75315	0.000344	0.00019	0.010841	-0.64335	HSRNASEB
253 g at	L42324	0.000344	0.00019	0.000262	-0.31758	HUMFRCG
32332 at	X69433	0.001377	0.00019	0.002925	0.209735	IDH2
36709 at	Y00093	0.000344	0.00019	2.60E-05	-0.39318	ITGAX
39080 at	M88458	0.001377	0.00019	0.002031	-0.15998	KDEL2
36545 s at	AB011114	0.000344	0.00019	3.13E-05	0.278271	KIAA0542
38915 at	AB011135	0.000344	0.00019	0.000149	0.247752	KIAA0563
40672 at	U57721	0.001377	0.00019	3.47E-05	-0.23188	KYNU
39441 at	Y11395	0.001377	0.00019	8.58E-05	0.34059	LANCL1
41590 at	AI652660	0.000344	0.00019	2.28E-05	0.385107	LOC51112
32350 at	AB026118	0.001377	0.00019	4.47E-06	-0.24886	MALT1
40469 at	AB011144	0.000344	0.00019	9.36E-05	0.26851	MCM3AP
41696 at	AI620381	0.000344	0.00019	8.06E-06	0.29605	MGC3077
38655 at	AI525633	0.000344	0.00019	2.44E-05	0.170916	MGC5576
40074 at	X16396	0.000344	0.00019	3.27E-06	-0.6151	MTHFD2

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37724_at	V00568	0.000344	0.00019	0.000769	0.549224	MYC
31896_at	AL050281	0.000344	0.00019	2.85E-06	0.30517	NAG
40686_at	AI985272	0.000344	0.00019	0.000474	-0.2571	NMB
31794_at	D38524	0.000344	0.00019	0.001313	0.228851	NT5B
34491_at	AJ225089	0.000344	0.00019	0.000531	-0.2589	OASL
36413_at	Z82200	0.000344	0.00019	0.000136	-0.28579	P2Y10
40791_at	X63564	0.001377	0.00019	1.70E-05	-0.28202	POLR2A
32157_at	S57501	0.001377	0.00019	0.002179	0.267744	PPP1CA
1217_g_at	X07109	0.000344	0.00019	0.000694	0.167774	PRKCB1
1074_at	M28209	0.000344	0.00019	0.000392	-0.52456	RAB1
1055_g_at	M87339	0.000344	0.00019	3.41E-05	0.248151	RFC4
35685_at	Z14000	0.000344	0.00019	3.91E-06	-0.33734	RING1
40875_s_at	X06815	0.000344	0.00019	3.50E-05	0.293968	SNRP70
37757_at	L23959	0.000344	0.00019	1.82E-05	-0.36834	TFDP1
32853_at	AB018262	0.000344	0.00019	0.000241	0.319056	TOMM70A
32793_at	X00437	0.001377	0.00019	0.00022	0.248344	TRB@
35214_at	AF061016	0.000344	0.00019	0.000264	0.349913	UGDH
38337_at	U62392	0.000344	0.00019	2.74E-05	-0.65983	ZNF193
34544_at	X78925	0.001377	0.00019	0.001253	-0.28003	ZNF267
39932_at	AI655015	0.001377	0.00019	0.00444	0.74681	
32672_at	AL049387	0.001377	0.00019	5.12E-06	0.379296	
41219_at	AL050376	0.000344	0.00019	0.00026	0.410405	
34435_at	AB008775	0.000344	0.000304	1.88E-06	-0.80745	AQP9
40175_at	AI141670	0.000344	0.000304	1.60E-06	-0.2494	CLCN2
35715_at	AL080071	0.000344	0.000304	3.12E-06	0.237367	DKFZP564M082
35163_at	AB028964	0.000344	0.000304	5.07E-05	0.351352	KIAA1041
33249_at	M16801	0.001377	0.000304	0.000458	0.412733	NR3C2
39131_at	N36842	0.001377	0.000304	0.000577	0.172944	UPF3A
33418_at	AL096752	0.000344	0.000304	0.000323	-0.20419	
38748_at	U76421	0.000344	0.000402	0.000278	0.226301	ADARB1
40745_at	L13939	0.001377	0.000402	0.000215	0.180874	APIB1
39347_at	X97074	0.001377	0.000402	0.001924	0.298218	AP2S1
818_s_at	U72936	0.000344	0.000402	1.03E-05	0.356824	ATRX
36945_at	X94910	0.000344	0.000402	0.000204	0.249294	C12orf8
40404_s_at	U18291	0.000344	0.000402	2.45E-05	0.594377	CDC16
1273_r_at	L22005	0.001377	0.000402	0.000111	-0.15257	CDC34
32833_at	M59287	0.00482	0.000402	0.000276	-0.72279	CLK1
35319_at	U25435	0.000344	0.000402	0.000648	0.264876	CTCF
630_at	L39874	0.000344	0.000402	2.41E-05	0.211923	DCTD
34647_at	X52104	0.000344	0.000402	0.000159	0.317963	DDX5
33776_at	AL050062	0.000344	0.000402	0.000377	0.36401	DKFZP566K023
35799_at	AL080081	0.00482	0.000402	0.000103	-0.60871	DNAJB9
40375_at	X63741	0.001377	0.000402	0.000175	-0.59207	EGR3
777_at	D13988	0.001377	0.000402	0.000371	0.14676	GDI2
1368_at	M27492	0.000344	0.000402	2.01E-06	-0.32619	IL1R1
33411_g_at	S66213	0.000344	0.000402	9.56E-05	0.247863	ITGA6

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34318 at	AJ005896	0.000344	0.000402	5.38E-05	0.210462	JM4
35472 at	Y10745	0.00482	0.000402	6.39E-05	-0.30524	KCNJ15
34837 at	AB002374	0.00482	0.000402	0.000916	0.20284	KIAA0376
41695 at	AB007874	0.001377	0.000402	0.000181	-0.21662	KIAA0414
33223 at	AB011133	0.00482	0.000402	0.000521	0.302843	KIAA0561
39339 at	AB018335	0.00482	0.000402	9.03E-05	0.234274	KIAA0792
37377 i at	M13452	0.00482	0.000402	0.00148	-0.28339	LMNA
32571 at	X68836	0.00482	0.000402	2.15E-05	-0.57967	MAT2A
37577 at	U79256	0.000344	0.000402	2.24E-05	0.328028	MGC14258
37181 at	X76538	0.001377	0.000402	5.62E-05	0.408464	MPV17
36537 at	AB011093	0.000344	0.000402	0.000101	0.612928	P114-RHO-GEF
1224 at	X66363	0.001377	0.000402	6.80E-05	-0.24041	PCTK1
41461 at	U13695	0.00482	0.000402	2.31E-05	0.31531	PMS1
35359 at	D87078	0.000344	0.000402	3.88E-05	0.497225	PUM2
109 at	Z97074	0.001377	0.000402	3.97E-05	0.296662	RAB9P40
39989 at	X90530	0.000344	0.000402	3.52E-05	0.254197	RAGB
36913 at	U75679	0.001377	0.000402	0.000139	-0.29594	SLBP
38764 at	AF007142	0.000344	0.000402	3.15E-06	0.678734	
36711 at	AL021977	0.00482	0.000402	8.82E-05	-0.82538	
38630 at	AL080192	0.001377	0.000402	4.26E-05	0.201319	
956 at	HG1980- HT2023	0.00482	0.000402	0.003775	-0.48359	
34003 at	U47924	0.001377	0.000402	0.000134	0.52195	
1933 g at	U83661	0.000344	0.000444	9.97E-06	0.270218	ABCC5
39700 at	AI961929	0.000344	0.000444	1.88E-05	0.461528	ARHGAP1
39649 at	X78817	0.000344	0.000444	2.82E-05	0.281835	ARHGAP4
34409 at	AL080164	0.000344	0.000444	0.000218	0.268161	DKFZP564C1940
37213 at	X90392	0.000344	0.000444	0.000208	0.150242	DNASE1L1
40859 at	AI561196	0.000344	0.000444	0.000156	0.302434	FLJ11806
37100 at	AJ008112	0.000344	0.000444	0.000246	-0.32126	FMNL
38016 at	M94630	0.000344	0.000444	0.000244	0.274532	HNRPD
35721 at	M38180	0.000344	0.000444	0.003037	-0.15741	HSD3B1
31838 at	U79274	0.000344	0.000444	9.67E-05	0.285563	HSU79274
40224 s at	AB014585	0.000344	0.000444	6.48E-05	0.460196	KIAA0685
34688 at	AB029001	0.000344	0.000444	0.000183	-0.33324	KIAA1078
32733 at	AA045160	0.000344	0.000444	4.62E-05	0.179556	MRPS14
40817 at	M96824	0.000344	0.000444	2.18E-05	0.139326	NUCB1
381 s at	Y10055	0.000344	0.000444	9.91E-06	0.176067	PIK3CD
38022 s at	Z54367	0.000344	0.000444	1.30E-05	-0.39738	PLEC1
34797 at	AF014402	0.000344	0.000444	7.63E-05	0.147061	PPAP2A
40513 at	M30773	0.000344	0.000444	0.001161	0.41229	PPP3R1
878 s at	M29386	0.000344	0.000444	6.26E-05	-0.23554	PRL
1852 at	X02910	0.000344	0.000444	0.001378	-0.17579	TNF
34916 s at	S76792	0.000344	0.000444	0.000211	-0.16737	TNFRSF4
37686 s at	Y09008	0.000344	0.000444	0.000352	0.168444	UNG
40147 at	U18009	0.000344	0.000444	0.002896	0.204706	VATI

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1307 at	D14533	0.000344	0.000444	0.000837	0.246085	XPA
36564 at	W27419	0.000344	0.000444	2.83E-05	-0.44121	
35001 at	Z85986	0.000344	0.000444	0.000407	-0.2149	
36607 at	Z99716	0.000344	0.000444	5.14E-05	0.324642	
35364 at	U50939	0.001377	0.000525	1.19E-05	0.235552	APPBP1
36554 at	Y15521	0.00482	0.000525	0.000492	-0.28889	ASMTL
37948 at	J05682	0.00482	0.000525	0.000291	-0.33004	ATP6C
37947 at	D26362	0.00482	0.000525	0.000707	0.247252	BRD3
39525 at	AL120687	0.001377	0.000525	1.21E-05	-0.55731	CSH1
40646 at	U20350	0.00482	0.000525	0.010386	0.383475	CX3CR1
37975 at	X04011	0.00482	0.000525	0.000154	0.348439	CYBB
36573 at	U78524	0.001377	0.000525	6.56E-05	-0.36872	DDXBP1
39182 at	U87947	0.001377	0.000525	5.05E-05	-0.29673	EMP3
39876 at	AL035252	0.00482	0.000525	0.003735	0.074075	ENTPD6
37307 at	X04828	0.00482	0.000525	0.0015	0.256297	GNAI2
32321 at	X56841	0.001377	0.000525	4.37E-05	0.338907	HLA-E
1185 at	D49410	0.00482	0.000525	0.00016	-0.21753	HUMIL3RA12
40815 g at	L40586	0.00482	0.000525	3.02E-05	-0.20891	IDS
37603 at	X52015	0.00482	0.000525	0.00032	-0.54051	IL1RN
37651 at	D31888	0.00482	0.000525	7.50E-06	-0.44687	KIAA0071
38394 at	D42047	0.001377	0.000525	3.50E-05	0.226884	KIAA0089
35442 at	AB007958	0.00482	0.000525	0.00023	0.259725	KIAA0489
35252 at	AB011100	0.00482	0.000525	0.000193	0.418151	KIAA0528
31803 at	AB014553	0.00482	0.000525	0.002002	-0.25439	KIAA0653
37308 at	AI888084	0.001377	0.000525	3.57E-05	0.391754	KIAA1624
32184 at	X61118	0.00482	0.000525	0.001631	0.292879	LMO2
34874 at	AJ004832	0.00482	0.000525	0.001715	0.30393	NTE
41665 at	AB020631	0.001377	0.000525	0.000212	0.379354	PCF11
37143 s at	AB002359	0.00482	0.000525	2.36E-05	0.271468	PFAS
37111 g at	AB012229	0.001377	0.000525	0.000168	-0.59579	PFKFB3
32210 at	M83088	0.001377	0.000525	3.50E-05	0.439367	PGM1
37392 at	X84908	0.001377	0.000525	2.25E-05	0.331887	PHKB
40624 at	U48250	0.001377	0.000525	8.51E-05	-0.2234	PRKCBP2
41853 at	AB007851	0.000344	0.000525	1.95E-05	0.481768	PRPSAP2
32070 at	X97267	0.00482	0.000525	0.000303	0.211707	PTPRCAP
32737 at	M64595	0.00482	0.000525	0.004436	0.170959	RAC2
36575 at	S59049	0.001377	0.000525	0.000915	-0.61362	RGS1
34714 at	AL050267	0.00482	0.000525	0.000204	0.311003	SAMHD1
41451 s at	W28498	0.00482	0.000525	1.70E-05	-0.57386	SAR1
41199 s at	W27050	0.00482	0.000525	2.37E-05	-0.587	SFPQ
37278 at	X92762	0.00482	0.000525	0.000116	0.283179	TAZ
34741 at	U18422	0.001377	0.000525	0.000279	-0.14486	TFDP2
950 at	D87127	0.001377	0.000525	0.000126	-0.32216	TLOC1
1468 at	U12595	0.001377	0.000525	1.07E-05	0.347309	TRAP1
40066 at	AF046024	0.00482	0.000525	0.000469	0.405378	UBE1C
32236 at	AF032456	0.001377	0.000525	5.89E-05	0.269833	UBE2G2

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41532 at	Y09723	0.00482	0.000525	0.000854	-0.23772	ZNF151
33297 at	AL031778	0.00482	0.000525	0.000239	0.178561	
36212 at	AL049218	0.00482	0.000525	0.001951	0.238837	
35187 at	AL080216	0.00482	0.000525	0.000349	0.311531	
32855 at	L00352	0.00482	0.000525	0.005084	-0.39882	
856 at	S79267	0.00482	0.000525	0.000908	-0.19945	
31615 i at	U94902	0.00482	0.000525	0.002556	-0.17833	
33198 at	AA206524	0.000344	0.000567	0.000172	0.161868	BART1
37347 at	AA926959	0.000344	0.000567	8.47E-05	0.169915	CKS1
876 at	M27543	0.000344	0.000567	0.000319	-0.48924	GNAI3
41556 s at	AF019386	0.000344	0.000567	0.000399	-0.18103	HS3ST1
38546 at	AB006537	0.000344	0.000567	0.000658	-0.1547	IL1RAP
38145 at	AJ001306	0.000344	0.000567	5.70E-05	0.338818	INADL
32235 at	AB011116	0.000344	0.000567	0.000355	0.25593	KIAA0544
33924 at	AB029014	0.000344	0.000567	0.001352	-0.1261	KIAA1091
34839 at	AB029027	0.000344	0.000567	0.00209	0.180974	KIAA1104
36690 at	M10901	0.000344	0.000567	4.00E-05	-0.42455	NR3C1
352 at	D30036	0.000344	0.000567	5.62E-05	-0.15539	PITPN
40129 at	U47077	0.000344	0.000567	0.001173	0.30799	PRKDC
33212 at	AF006751	0.000344	0.000567	3.40E-05	-0.23462	RRBP1
33706 at	AB006198	0.000344	0.000567	0.001465	0.256734	SART1
40104 at	D63780	0.000344	0.000567	0.00021	0.374406	STK25
33850 at	W28892	0.000344	0.000567	8.26E-05	0.803602	SUI1
890 at	M74524	0.000344	0.000567	0.000421	-0.31531	UBE2A
41790 at	AL031230	0.000344	0.000567	6.83E-05	0.272378	
37303 at	AF057160	0.001377	0.000588	0.000279	0.307281	ADPRTL1
39336 at	M74491	0.001377	0.000588	3.02E-05	0.170825	ARF3
36872 at	AL120559	0.001377	0.000588	4.80E-05	-0.64478	ARPP-19
40108 at	D13630	0.001377	0.000588	3.01E-05	-0.42457	BZAP45
40452 at	U83246	0.001377	0.000588	0.003502	0.133045	CPNE1
31852 at	AL050390	0.001377	0.000588	0.000139	0.231898	DKFZP564O043
36201 at	D13315	0.001377	0.000588	0.000203	0.371377	GLO1
2090 i at	H12458	0.001377	0.000588	5.42E-05	-0.22578	H12458 yj12d03.sl
35738 at	A1347088	0.001377	0.000588	0.000151	0.321012	HMG17L3
998 s at	X59770	0.001377	0.000588	0.001417	-0.36292	IL1R2
40461 at	AB007855	0.000344	0.000588	1.02E-05	0.086396	KIAA0395
36213 at	AB016816	0.001377	0.000588	0.000751	0.146218	MASL1
518 at	U07132	0.001377	0.000588	0.002035	-0.27336	NR1H2
35835 at	AB019409	0.001377	0.000588	0.001479	0.154377	PDL-108
36502 at	AB020641	0.001377	0.000588	0.00342	0.174568	PFTK1
40521 at	AL050259	0.001377	0.000588	0.001864	0.272972	RAB2L
35236 g at	AA099265	0.001377	0.000588	0.000614	0.38275	RECK
1856 at	X75042	0.001377	0.000588	6.85E-05	-0.39572	REL
34304 s at	AL050290	0.001377	0.000588	0.002426	-0.28771	SAT
39399 at	AJ006417	0.001377	0.000588	0.000125	-0.18595	TBCD



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41445 at	X02812	0.001377	0.000588	1.78E-05	-0.16423	TGFB1
36243 at	AL050262	0.001377	0.000588	0.0031	0.348226	TLR1
33616 at	X16576	0.001377	0.000588	9.49E-05	0.431692	ZNF46
41362 at	X91249	0.000344	0.000609	1.04E-05	-0.3925	ABCG1
34310 at	Y00486	0.000344	0.000609	0.000297	0.259418	APRT
32772 s at	U10473	0.000344	0.000609	0.000103	-0.15424	B4GALT1
40141 at	AB014595	0.000344	0.000609	5.19E-05	0.320955	CUL4B
33791 at	Y15227	0.000344	0.000609	4.08E-05	0.222481	DLEU1
32168 s at	U85267	0.000344	0.000609	0.000131	0.142894	DSCR1
35296 at	AB019036	0.000344	0.000609	0.000336	0.177649	GGPS1
824 at	U90313	0.000344	0.000609	0.001838	-0.25377	GSTTLp28
1589 s at	L42243	0.000344	0.000609	0.000201	0.403838	HUMIFNAM08
35731 at	X16983	0.000344	0.000609	0.000317	0.232935	ITGA4
35830 at	AB002368	0.000344	0.000609	0.001709	0.215217	KIAA0370
36171 at	AI521453	0.000344	0.000609	0.000707	-0.22735	PC4
32140 at	Y08110	0.000344	0.000609	9.87E-05	0.260436	SORL1
1858 at	D38122	0.000344	0.000609	6.27E-05	-0.61781	TNFSF6
36959 at	U49278	0.000344	0.000609	0.000173	0.204424	UBE2V1
39429 at	X99050	0.000344	0.000609	7.72E-05	0.289751	UVRAG
39756 g at	Z93930	0.000344	0.000609	0.00015	-0.26558	XBPI
38053 s at	AF015767	0.000344	0.000659	0.000199	0.578977	BRE
37907 at	M34677	0.000344	0.000659	0.000647	0.198622	F8A
1666 at	J00210	0.000344	0.000659	0.002453	-0.18828	IFNA1
41346 at	AJ007583	0.000344	0.000659	0.00506	-0.12644	LARGE
2059 s at	M36881	0.000344	0.000659	0.000302	0.328248	LCK
36174 at	X70326	0.000344	0.000659	0.000132	-0.58974	MACMARCKS
32226 at	M64571	0.000344	0.000659	0.000158	0.157573	MAP4
38605 at	AI345944	0.000344	0.000659	0.000363	0.311507	NDUFB1
1695 at	D23662	0.000344	0.000659	0.000171	0.289452	NEDD8
38590 r at	M14630	0.000344	0.000659	1.26E-05	-0.1626	PTMA
41763 g at	D64015	0.000344	0.000659	0.001012	0.195679	TIAL1
32323 at	M63582	0.000344	0.000659	2.66E-05	-0.39175	
35564 at	U79300	0.000344	0.000659	0.000196	-0.16218	
40960 at	D29805	0.00482	0.000812	0.000289	-0.23044	B4GALT1
1913 at	U47414	0.001377	0.000812	0.000137	0.262974	CCNG2
266 s at	L33930	0.001377	0.000812	5.56E-06	0.343203	CD24
32111 at	AL050164	0.00482	0.000812	0.000345	0.307729	CDYL
40082 at	D10040	0.001377	0.000812	1.49E-05	-0.45708	FACL2
37187 at	M36820	0.00482	0.000812	7.67E-05	-0.49075	GRO2
466 at	U77948	0.00482	0.000812	0.000511	0.286776	GTF2I
41484 r at	X56681	0.00482	0.000812	0.000503	-0.18359	JUND
35224 at	AF070569	0.00482	0.000812	0.000446	-0.6104	MGC14376
34258 at	W28205	0.00482	0.000812	0.00017	-0.21741	MKLN1
1719 at	U61981	0.001377	0.000812	0.000725	0.203996	MSH3
39707 at	AB014547	0.001377	0.000812	7.73E-05	0.217806	MTMR4
39507 at	AL050366	0.00482	0.000812	0.001126	0.421541	OGT

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35714_at	U89606	0.001377	0.000812	6.13E-05	-0.19512	PDXK
1810_s_at	D10495	0.00482	0.000812	0.000433	0.290156	PRKCD
32788_at	D42063	0.001377	0.000812	0.000346	-0.52828	RANBP2
41446_f_at	H68340	0.00482	0.000812	0.004081	-0.3419	RNAHP
41544_at	AF059617	0.001377	0.000812	0.00012	-0.27807	SNK
32166_at	AB028950	0.00482	0.000812	0.000365	0.313606	TLN1
1729_at	L41690	0.001377	0.000812	0.000109	0.401776	TRADD
32173_at	X95384	0.00482	0.000812	0.00053	0.327055	UK114
36000_at	X98054	0.00482	0.001094	4.71E-05	-0.12615	CREBL1
271_s_at	J05036	0.00482	0.001094	0.00171	0.064463	CTSE
40098_at	AF001434	0.00482	0.001094	0.000161	-0.26223	EHD1
663_at	L18960	0.00482	0.001094	3.26E-05	-0.38369	EIF1A
38340_at	AB014555	0.00482	0.001094	0.001608	-0.18202	KIAA0655
36673_at	X76057	0.00482	0.001094	0.000352	0.193745	MPI
1986_at	X74594	0.00482	0.001094	0.000352	0.439326	RBL2
39857_at	AF044309	0.00482	0.001094	0.000217	-0.2163	STX11
37911_at	U07158	0.00482	0.001094	0.000122	-0.2301	STX4A
633_s_at	L40386	0.00482	0.001094	7.97E-05	-0.19863	TFDP2
39518_at	H97470	0.00482	0.001094	0.000624	-0.10587	
38213_at	U78027	0.00482	0.001094	0.000804	0.340784	
1530_g_at	U50534	0.001377	0.001345	0.00039	0.250627	13CDNA73
34181_at	X55330	0.001377	0.001345	9.30E-05	0.493025	AGA
36637_at	L19605	0.001377	0.001345	0.004442	0.183134	ANXA11
39082_at	Y00097	0.001377	0.001345	4.42E-05	0.409932	ANXA6
2000_at	U26455	0.00482	0.001345	0.000705	0.499049	ATM
34783_s_at	AF047473	0.001377	0.001345	5.14E-05	0.226	BUB3
579_at	M95724	0.00482	0.001345	0.002166	-0.46553	CENPC1
35852_at	AB014558	0.001377	0.001345	0.004662	-0.44793	CRY2
41670_at	R38263	0.001377	0.001345	0.00048	-0.12843	DJ347H13.4
36403_s_at	A1434146	0.001377	0.001345	0.000397	0.187485	DKFZp57010164
1306_at	D12686	0.00482	0.001345	0.008744	-0.11456	EIF4G1
39542_at	AF059611	0.00482	0.001345	0.000694	-0.27343	ENC1
40522_at	X59834	0.001377	0.001345	0.004986	-0.34836	GLUL
319_g_at	D64142	0.001377	0.001345	0.000169	0.293999	H1FX
36372_at	U51333	0.001377	0.001345	0.000376	0.273402	HK3
235_at	M59488	0.001377	0.001345	0.001357	-0.13313	HUMS100B3
41166_at	X58529	0.001377	0.001345	0.000417	1.04789	IGHM
37695_at	D79983	0.001377	0.001345	2.97E-05	0.387491	KIAA0161
40517_at	AB002370	0.00482	0.001345	0.00052	0.425557	KIAA0372
33333_at	AB007863	0.001377	0.001345	0.000128	0.29668	KIAA0403
39580_at	AB014549	0.001377	0.001345	0.001505	0.42387	KIAA0649
37772_at	AB020711	0.00482	0.001345	0.002079	0.222346	KIAA0904
34713_at	AB002357	0.001377	0.001345	0.001045	0.317849	KIF3B
39232_at	U09284	0.00482	0.001345	0.000792	-0.23635	LIMS1
35421_at	D50810	0.001377	0.001345	5.17E-05	-0.1859	LNPEP
41511_at	U18259	0.001377	0.001345	0.000153	0.229322	MHC2TA

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40877 s at	AF041080	0.00482	0.001345	0.001964	0.367098	MN7
40405 at	X70991	0.001377	0.001345	0.00203	-0.14032	NAB2
33836 at	AC002045	0.00482	0.001345	0.00028	0.326033	NPIP
38155 at	U92538	0.001377	0.001345	0.00149	0.2372	ORC5L
1560 g at	U24153	0.001377	0.001345	0.00018	-0.36291	PAK2
36239 at	Z49194	0.001377	0.001345	0.000519	0.215733	POU2AF1
38352 at	AF016371	0.001377	0.001345	0.001059	0.240562	PPIH
32848 at	AF020736	0.001377	0.001345	6.26E-05	-0.32893	PSMC4
1760 s at	D11327	0.001377	0.001345	0.00019	-0.74969	PTPN7
35255 at	AF098799	0.00482	0.001345	0.001893	-0.3646	RANBP7
1848 at	M22995	0.001377	0.001345	0.005586	0.270032	RAP1A
31546 at	L11566	0.001377	0.001345	0.000291	0.17032	RPL18
34438 at	U71364	0.001377	0.001345	0.000276	-0.24064	SERPINB9
34666 at	X07834	0.00482	0.001345	0.000362	-0.21917	SOD2
1634 s at	X05839	0.001377	0.001345	0.000779	-0.20819	TGFB1
35238 at	AB000509	0.001377	0.001345	3.63E-05	0.460686	TRAF5
147 at	U82130	0.001377	0.001345	4.69E-05	-0.36064	TSG101
283 at	L16842	0.001377	0.001345	0.001533	0.189597	UQCRC1
40103 at	X51521	0.001377	0.001345	0.000379	-0.62845	VIL2
1235 at	M86400	0.001377	0.001345	0.000132	-0.30595	YWHAZ
32034 at	AF041259	0.001377	0.001345	0.001393	0.202001	ZNF217
34906 g at	AA977136	0.001377	0.001345	0.001953	0.095364	
36230 at	AI624038	0.001377	0.001345	0.001833	-0.16137	
35645 at	AL050148	0.00482	0.001345	0.000905	0.266795	
1285 at	HG2709- HT2805	0.001377	0.001345	0.000134	-0.22645	
1162 g at	HG3227- HT3404	0.001377	0.001345	4.02E-05	-0.23244	
34375 at	M28225	0.00482	0.001345	0.001444	-0.95152	
37277 at	U80017	0.001377	0.001345	0.004917	0.171432	
36297 at	X55544	0.001377	0.001467	0.001049	-0.12406	ATF1
38354 at	X52560	0.001377	0.001467	8.17E-05	-0.50375	CEBPB
41360 at	AA044787	0.001377	0.001467	0.001147	0.289086	CNOT8
40041 at	AF017790	0.001377	0.001467	6.88E-06	0.382661	HEC
771 s at	D00749	0.001377	0.001467	0.000131	-0.10539	HUMCD7G3
31936 s at	AB007890	0.001377	0.001467	0.000838	0.200677	KIAA0430
36371 at	L35251	0.001377	0.001467	0.000873	0.12909	MFAP3
32742 s at	AF098638	0.001377	0.001467	0.000684	-0.18761	RAB5EP
35320 at	AB004857	0.001377	0.001467	0.000471	0.23048	SLC11A2
41778 at	U53347	0.001377	0.001467	0.001367	-0.13658	SLC1A5
40416 at	U04847	0.001377	0.001467	0.000403	0.117176	SMARCB1
40448 at	M92843	0.001377	0.001467	3.30E-05	-1.37866	ZFP36
34001 at	AF033199	0.001377	0.001467	0.00019	0.237743	ZNF204
37504 at	AC004893	0.001377	0.001467	0.000617	-0.25759	
38505 at	AL050151	0.001377	0.001467	8.03E-06	-0.80887	
31771 at	U80770	0.001377	0.001467	0.006738	-0.12644	
31665 s at	W27675	0.00482	0.001614	0.005157	0.468709	CDA02

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35233 r at	AI056696	0.00482	0.001614	0.000665	0.215941	CETN3
39723 at	AF062536	0.00482	0.001614	0.005001	0.197482	CUL1
38791 at	D29643	0.00482	0.001614	0.0005	0.157183	DDOST
35972 at	AA181196	0.00482	0.001614	0.000166	0.119162	FLJ11712
35261 at	W07033	0.001377	0.001614	0.000136	0.347648	GMFG
34571 at	Z18859	0.00482	0.001614	0.000684	0.181514	GNAT2
1931 at	U83660	0.00482	0.001614	0.00114	0.136411	HSU83660
38828 s at	AA628946	0.00482	0.001614	0.002684	0.337197	KHSRP
33462 at	D13626	0.00482	0.001614	0.005837	0.254138	KIAA0001
32660 at	AB002340	0.00482	0.001614	0.002977	0.168464	KIAA0342
32208 at	AB002353	0.001377	0.001614	0.000119	0.305921	KIAA0355
36472 at	U32849	0.00482	0.001614	0.000272	0.345048	NMI
1348 s at	S79219	0.00482	0.001614	0.000119	0.167463	PCCA
1486 at	L37127	0.00482	0.001614	0.010173	0.103446	POLR2J
32776 at	M35416	0.00482	0.001614	0.001433	0.33505	RALB
32597 at	X76061	0.00482	0.001614	0.000273	0.378113	RBL2
40782 at	AF061741	0.00482	0.001614	0.004586	0.221278	SDR1
34189 at	D31891	0.001377	0.001614	0.000819	0.161458	SETDB1
32161 at	W26406	0.00482	0.001614	0.000479	0.300512	SLAH1
802 at	X84002	0.00482	0.001614	0.000699	0.143479	TAF2J
34307 at	U81006	0.00482	0.001614	0.003151	0.255479	TM9SF2
1328 at	U69108	0.00482	0.001614	0.000657	0.208286	TRAF5
31618 at	S66666	0.00482	0.001614	0.002417	0.119478	
1211 s at	U84388	0.00482	0.001719	0.000197	-0.18606	CRADD
39118 at	L08069	0.00482	0.001719	0.001985	-0.31866	DNAJA1
38041 at	U41514	0.00482	0.001719	9.38E-05	-0.44803	GALNT1
40562 at	M69013	0.001377	0.001719	6.26E-05	-0.1948	GNA11
38320 s at	L11706	0.00482	0.001719	0.001422	-0.16675	LIPE
36130 f at	R92331	0.00482	0.001719	0.000198	-0.24196	MT1E
37544 at	X64318	0.00482	0.001719	0.006253	-0.37391	NFIL3
40360 at	X12458	0.00482	0.001719	0.001489	-0.33668	P3
1265 g at	M25393	0.00482	0.001719	0.000958	-0.23304	PTPN2
595 at	M59465	0.00482	0.001719	0.0002	-0.96074	TNFAIP3
34323 at	AF084260	0.00482	0.001719	0.001063	-0.39491	TRIP15
733 at	HG2149- HT2219	0.00482	0.001719	0.001437	-0.14432	
39158 at	AB021663	0.00482	0.001963	0.00027	-0.13923	ATF5
39692 at	AL080209	0.00482	0.001963	0.000337	0.437957	DKFZP586F2423
2056 at	M34641	0.00482	0.001963	0.002352	-0.14552	FGFR1
38710 at	AL096714	0.001377	0.001963	0.000469	0.224782	FLJ20113
38248 at	AB011124	0.001377	0.001963	0.000101	-0.17709	KIAA0552
40492 at	AB020633	0.001377	0.001963	0.00082	0.308616	KIAA0826
33219 at	AB029020	0.001377	0.001963	0.00061	0.3824	KIAA1097
38051 at	X76220	0.001377	0.001963	7.21E-05	0.444366	MAL
34482 at	AF040964	0.00482	0.001963	0.001161	-0.54746	MGC4701
41475 at	U91512	0.001377	0.001963	0.00035	-0.55826	NINJ1

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1014 at	U60325	0.00482	0.001963	0.000288	-0.14386	POLG
362 at	Z15108	0.001377	0.001963	0.000107	0.176424	PRKCZ
36998 s at	Y08262	0.001377	0.001963	0.000183	0.377974	SCA2
37423 at	U30246	0.001377	0.001963	0.000209	-0.25952	SLC12A2
35293 at	J04137	0.001377	0.001963	0.000641	-0.22175	SSA2
1830 s at	M38449	0.001377	0.001963	0.0004	-0.29059	TGFB1
36531 r at	AC005757	0.00482	0.001963	0.000169	0.387439	
919 at	HG825- HT825	0.001377	0.001963	0.000553	-0.19964	
39590 at	AF047348	0.001377	0.002207	0.000292	0.202669	APBA2
31877 at	AF053977	0.001377	0.002207	0.003143	0.134266	CDC23
38345 at	AF083322	0.001377	0.002207	0.000344	0.272282	CEP1
40905 s at	AL050369	0.001377	0.002207	0.001224	0.241992	DKFZP566J153
36188 at	D32257	0.001377	0.002207	0.000238	0.300058	GTF3A
32087 at	M65217	0.001377	0.002207	0.000232	0.249614	HSF2
31826 at	AB014574	0.001377	0.002207	0.000606	0.130056	KIAA0674
41179 at	AB029023	0.001377	0.002207	0.000219	0.219428	KIAA1100
38390 at	Z34975	0.001377	0.002207	8.88E-05	0.41432	LDLC
40715 at	D83597	0.001377	0.002207	0.000136	0.249838	LY64
38431 at	U09759	0.001377	0.002207	0.000842	0.330751	MAPK9
484 at	U59302	0.001377	0.002207	0.000241	0.309348	NCOA1
36003 at	AJ005698	0.001377	0.002207	0.004173	0.139618	PARN
37362 at	X54871	0.001377	0.002207	0.010035	0.119258	RAB5B
35722 at	AL080198	0.001377	0.002207	0.002866	0.251598	RENT2
39988 at	M74447	0.001377	0.002207	0.000444	0.093537	TAP2
40854 at	J04973	0.001377	0.002207	0.011696	0.141705	UQCRC2
38370 at	U90902	0.001377	0.002207	0.001336	0.246217	
35036 at	U94333	0.001377	0.002323	0.004818	-0.13898	C1QR
40218 at	U60808	0.001377	0.002323	0.000374	-0.12217	CDS1
276 at	L08069	0.001377	0.002323	0.002161	-0.29982	DNAJA1
38706 at	AA552140	0.001377	0.002323	0.003368	-0.22604	E2F4
587 at	M31210	0.001377	0.002323	0.000124	-0.33555	EDG1
37018 at	A1189287	0.001377	0.002323	0.002445	-0.24115	H1F2
33363 at	W25934	0.001377	0.002323	0.003385	-0.32382	JTV1
34860 g at	Z98046	0.001377	0.002323	0.000122	-0.33551	MAGED2
37505 at	L76571	0.001377	0.002323	0.009985	-0.12617	NR0B2
39859 r at	AF071504	0.001377	0.002323	0.000191	-0.14267	STX11
38795 s at	X56687	0.001377	0.002323	0.00011	-0.29728	UBTF
38245 i at	A1097085	0.001377	0.002323	0.000941	-0.16209	
36633 at	AA114830	0.001377	0.002503	0.000293	0.272601	AKAP10
39094 at	A1991631	0.001377	0.002503	0.000132	-0.11786	BRD4
36270 at	U04343	0.001377	0.002503	4.45E-05	-0.25478	CD86
40699 at	M12824	0.001377	0.002503	0.008271	-0.34597	CD8A
446 at	U89896	0.001377	0.002503	0.006997	-0.2182	CSNK1G2
39593 at	A1432401	0.001377	0.002503	0.006072	0.32631	FGL2
40486 g at	AA176780	0.001377	0.002503	0.001296	0.14235	HSA249128

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31840 at	M21188	0.001377	0.002503	0.000165	0.251899	IDE
41596 s at	U43572	0.001377	0.002503	0.000128	0.318327	NAGLU
1539 at	X02751	0.001377	0.002503	0.000359	-0.2229	NRAS
34397 at	AF069250	0.001377	0.002503	0.00135	0.476217	OA48-18
39175 at	D25328	0.001377	0.002503	0.000171	0.125335	PFKP
37024 at	AF010312	0.001377	0.002503	0.001216	-0.47628	PIG7
1496 at	M34668	0.001377	0.002503	0.000421	0.181315	PTPRA
39601 at	AF061836	0.001377	0.002503	0.001026	0.21847	RASSF1
33369 at	AI535653	0.001377	0.002503	0.001712	0.34571	SC4MOL
36112 r at	X75755	0.001377	0.002503	0.003813	-0.2236	SFRS2
35270 at	W16505	0.001377	0.002503	0.001699	0.101763	SNRPD2
37074 at	L31529	0.001377	0.002503	0.000325	0.144265	SNTB1
36940 at	D86970	0.001377	0.002503	0.000219	0.218777	TIAF1
32254 at	AL050223	0.001377	0.002503	0.002632	0.2458	VAMP2
35916 s at	AA877215	0.001377	0.002503	0.008439	-0.17878	
38510 at	AL049435	0.001377	0.002503	0.000111	0.194323	
40201 at	M76180	0.001377	0.002575	0.000698	0.162775	DDC
33195 at	M94065	0.001377	0.002575	0.000426	0.156894	DHODH
1161 at	J04988	0.001377	0.002575	6.17E-05	-0.22304	HSPCB
36574 at	Z68907	0.001377	0.002575	0.000305	0.391111	IDH3G
39728 at	J03909	0.001377	0.002575	0.000837	-0.35709	IFI30
34192 at	AB011104	0.001377	0.002575	0.000729	0.227798	KIAA0532
41122 at	AB011173	0.001377	0.002575	0.000585	0.283714	KIAA0601
40463 at	U70322	0.001377	0.002575	0.000177	-0.41259	KPNB2
37542 at	D86961	0.001377	0.002575	0.001925	-0.19403	LHFPL2
38956 at	AF052111	0.001377	0.002575	0.000738	0.249468	LOC51172
32051 at	AJ224875	0.001377	0.002575	0.005091	0.139606	MGC2840
1406 at	M21985	0.001377	0.002575	0.001409	-0.102	NR2C1
1594 at	J05448	0.001377	0.002575	0.004982	-0.15329	POLR2C
38011 at	AB006572	0.001377	0.002575	0.000169	0.213636	RMP
36113 s at	AJ011712	0.001377	0.002575	0.011372	0.066711	TNNT1
39134 at	AJ006973	0.001377	0.002575	0.000101	-0.31773	TOM1
457 s at	U67122	0.001377	0.002575	0.000364	-0.14274	UBL1
40691 at	U71598	0.001377	0.002575	0.003508	0.128607	ZNF274
37707 i at	M81118	0.001377	0.002575	0.00023	0.333526	
488 at	U61166	0.001377	0.002575	0.003055	-0.14488	
31616 r at	U94902	0.001377	0.002575	0.000137	-0.23298	
33802 at	Z82244	0.001377	0.002575	0.000258	-0.53938	
36585 at	M36341	0.001377	0.002788	0.00056	-0.38498	ARF4
37309 at	L09159	0.001377	0.002788	0.00112	0.474985	ARHA
459 s at	U68485	0.00482	0.002788	0.006797	0.224774	BIN1
41200 at	Z22555	0.001377	0.002788	0.005455	-0.16351	CD36L1
38976 at	D44497	0.00482	0.002788	0.004453	0.131654	CORO1A
40184 at	L37042	0.00482	0.002788	0.000582	-0.33273	CSNK1A1
31823 at	M74099	0.001377	0.002788	0.00014	0.389638	CUTL1
35377 at	AL080159	0.001377	0.002788	0.002335	-0.11101	DKFZP434M154

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32807 at	AF004292	0.001377	0.002788	0.001306	-0.2375	DKFZP566C134
38632 at	AF088982	0.001377	0.002788	0.001264	-0.22098	DNAJB5
39983 at	U73704	0.001377	0.002788	0.001412	-0.17508	FAP48
1071 at	M77810	0.00482	0.002788	0.000209	-0.15854	GATA2
33977 at	U67369	0.00482	0.002788	0.00347	0.137095	GFI1
770 at	D00632	0.001377	0.002788	0.001138	-0.15517	GPX3
41838 at	X99270	0.001377	0.002788	0.00065	0.191612	HSXQ28ORF
37040 at	D42041	0.00482	0.002788	0.003705	0.195279	KIAA0088
34359 at	AA524058	0.001377	0.002788	0.000288	0.360599	LOC51020
820 at	U77604	0.001377	0.002788	0.00233	0.296247	MGST2
674 g at	J04031	0.00482	0.002788	0.000148	0.290038	MTHFD1
31883 at	AF025794	0.001377	0.002788	0.006763	0.107466	MTRR
37356 r at	D86326	0.001377	0.002788	0.008217	0.124987	P115
34254 at	U14417	0.001377	0.002788	0.000521	-0.13999	RALGDS
1020 s at	U85611	0.001377	0.002788	0.000126	-0.3879	SIP2-28
454 at	U66617	0.001377	0.002788	0.001462	-0.14653	SMARCD1
32574 at	X59960	0.001377	0.002788	0.005127	-0.11069	SMPD1
40262 at	AF031166	0.001377	0.002788	0.001219	0.110457	SRP46
1701 at	U86136	0.001377	0.002788	0.000542	0.149235	TEP1
37460 at	U16296	0.001377	0.002788	0.00138	0.136848	TIAM1
37312 at	D50917	0.001377	0.002788	0.000467	0.402091	TRIP-Br2
34224 at	AC004770	0.001377	0.002788	0.001042	-0.10615	
31493 s at	J03071	0.001377	0.002788	0.0116	0.17732	
33102 at	D67031	0.00482	0.004163	0.000204	0.543743	ADD3
458 at	U68030	0.00482	0.004163	0.000279	-0.16075	CCR6
40490 at	U41387	0.00482	0.004163	8.67E-05	-0.29576	DDX21
34249 at	AF084535	0.00482	0.004163	0.002306	0.159095	EPM2A
35988 i at	AI417075	0.00482	0.004163	0.000538	0.330385	FLJ14040
38811 at	D82348	0.00482	0.004349	0.006063	0.245422	ATIC
38084 at	AA648295	0.00482	0.004349	0.002422	0.337484	CBX3
34723 at	U79270	0.00482	0.004349	0.001345	0.460807	COX11
39846 at	AF071748	0.00482	0.004349	0.002471	0.170315	CTSF
40341 at	AL080088	0.00482	0.004349	0.000207	0.165357	DKFZP564K206 2
41234 at	AI540318	0.00482	0.004349	0.00055	-0.13789	DNAJB6
38012 at	U03272	0.00482	0.004349	0.003893	0.101031	FBN2
40479 at	Z97989	0.00482	0.004349	0.001126	-0.41969	FYN
39918 at	AF042379	0.00482	0.004349	0.008308	0.176604	GCP2
1017 at	U73737	0.00482	0.004349	0.00262	-0.14396	HUMMSH06
38488 s at	AF031167	0.00482	0.004349	0.000117	0.201914	IL15
34221 at	D83778	0.00482	0.004349	0.000504	-0.2149	KIAA0194
35789 at	AB028965	0.00482	0.004349	0.007277	0.125446	KIAA1042
2024 s at	M79321	0.00482	0.004349	0.003247	-0.21992	LYN
1130 at	L11284	0.00482	0.004349	0.003994	-0.09508	MAP2K1
36118 at	AJ000882	0.00482	0.004349	0.00042	0.180413	NCOA1
40822 at	L41067	0.00482	0.004349	0.000388	0.370635	NFATC3

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36146 at	AF057297	0.00482	0.004349	0.001191	0.521103	OAZ2
39873 at	X66360	0.00482	0.004349	0.001123	-0.17473	PCTK2
36196 at	U24183	0.00482	0.004349	0.001156	0.141168	PFKM
903 at	L42373	0.00482	0.004349	0.006706	0.165885	PPP2R5A
40824 at	AB018288	0.00482	0.004349	0.003777	0.184227	RANBP16
41214 at	M58459	0.00482	0.004349	0.008923	-1.04752	RPS4Y
2037 s at	M60725	0.00482	0.004349	0.001349	-0.10092	RPS6KB1
32402 s at	Y10931	0.00482	0.004349	0.001246	0.194156	SPK
40968 at	AB004904	0.00482	0.004349	0.000233	-0.31373	SSI-3
31868 at	AF060798	0.00482	0.004349	0.000809	0.142845	STK16
38480 s at	U66867	0.00482	0.004349	0.011318	0.150812	UBE2I
35847 at	AB028980	0.00482	0.004349	0.001471	0.265042	USP24
38262 at	AF052107	0.00482	0.004349	0.002884	0.197902	
35557 at	AL031985	0.00482	0.004349	0.000181	-0.24089	
35440 g at	D26121	0.00482	0.004349	0.00387	-0.16268	
34036 at	W28667	0.00482	0.004349	0.004391	0.476395	
34833 at	AL050157	0.00482	0.004467	0.000289	0.269949	DKFZP586O0120
38368 at	U31930	0.00482	0.004467	0.000244	0.349997	DUT
41338 at	AI951946	0.00482	0.004467	8.71E-05	0.401112	HBOA
35650 at	AB002354	0.00482	0.004467	0.001517	-0.13368	KIAA0356
1376 at	M36067	0.00482	0.004467	8.15E-05	0.277858	LIG1
691 g at	J02783	0.00482	0.004467	0.002151	-0.21979	P4HB
1085 s at	M37238	0.00482	0.004467	0.005333	-0.15474	PLCG2
38234 at	M99438	0.00482	0.004467	6.20E-05	-0.36844	TLE3
33386 at	Z97630	0.00482	0.004467	0.002794	0.217849	
34777 at	D14874	0.00482	0.005608	0.000611	-0.55358	ADM
931 at	L08177	0.00482	0.005608	0.000434	-0.49252	EBI2
36581 at	U09510	0.00482	0.005608	5.27E-05	-0.57567	GARS
1126 s at	L05424	0.00482	0.005608	0.000114	-0.39048	HUMSCG19
35135 at	X13956	0.00482	0.005608	0.004098	0.187622	MGC10471
38335 at	U88620	0.00482	0.005608	0.00074	0.345628	OGG1
39780 at	M29551	0.00482	0.005608	0.000471	0.319301	PPP3CB
39604 at	AF068836	0.00482	0.005608	0.000323	-0.23628	PSCDBP
33229 at	U08316	0.00482	0.005608	0.0006	0.205899	RPS6KA3
32822 at	J02966	0.00482	0.005608	0.000498	-0.11291	SLC25A4
38040 at	AF107463	0.00482	0.005608	0.002824	-0.36924	SPF30
33124 at	AB000450	0.00482	0.005608	0.000256	-0.24717	VRK2
40760 at	AF070590	0.00482	0.005608	0.000834	0.127523	
32238 at	AF001383	0.00482	0.006065	0.002075	0.16512	BIN1
32594 at	AF026291	0.00482	0.006065	0.000385	-0.16859	CCT4
37642 at	D63877	0.00482	0.006065	0.005226	-0.13956	KIAA0157
191 at	U14383	0.00482	0.006065	0.002623	-0.18669	MUC8
40285 at	U68140	0.00482	0.006065	0.000677	0.172443	NVL
1275 at	L25441	0.00482	0.006065	0.000613	-0.17207	PGGT1B
40898 at	U46751	0.00482	0.006065	0.000578	-0.38675	SQSTM1



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1149 at	HG4740-HT5187	0.00482	0.006065	0.00867	0.146562	
38864 at	W26851	0.00482	0.006065	0.002052	0.312992	
35183 at	U78735	0.00482	0.006347	0.000529	-0.09197	ABCA3
35274 at	Y12226	0.00482	0.006347	0.000397	-0.21303	AP1G1
37237 at	D38293	0.00482	0.006347	0.002894	-0.24373	AP3M2
31870 at	X14046	0.00482	0.006347	0.001084	0.134786	CD37
40174 at	AF026004	0.00482	0.006347	0.008622	-0.07494	CLCN2
38916 at	U46023	0.00482	0.006347	0.000273	-0.17969	CXorf6
39607 at	AL080178	0.00482	0.006347	0.000683	0.260343	DKFZP434K171
41437 at	AL080118	0.00482	0.006347	0.001904	-0.28696	DKFZP564F1123
34821 at	AL050197	0.00482	0.006347	0.004294	0.233045	DKFZP586D0623
1005 at	X68277	0.00482	0.006347	0.011411	-0.42385	DUSP1
38042 at	X03674	0.00482	0.006347	0.008478	0.174463	G6PD
35307 at	Y13286	0.00482	0.006347	0.004068	0.134985	GDI2
1038 s at	U19247	0.00482	0.006347	0.000589	-0.29688	HSINFGRA7
35973 at	AB023163	0.00482	0.006347	0.002537	0.194491	HYPH
36598 s at	L36818	0.00482	0.006347	0.007182	0.204818	INPPL1
36465 at	U51127	0.00482	0.006347	0.003952	0.108702	IRF5
37918 at	M15395	0.00482	0.006347	0.001863	0.402323	ITGB2
35755 at	U51336	0.00482	0.006347	0.008615	0.336527	ITPK1
39222 at	AJ000008	0.00482	0.006347	0.000256	-0.14181	PIK3C2G
33150 at	AI126004	0.00482	0.006347	0.000954	0.262925	SAS10
34432 at	AF051325	0.00482	0.006347	0.000144	-0.43952	SH2D2A
33879 at	U79528	0.00482	0.006347	0.002518	0.158101	SR-BP1
36900 at	U52426	0.00482	0.006347	9.31E-05	0.411984	STIM1
38113 at	AB018339	0.00482	0.006347	0.000751	0.199758	SYNE-1B
33873 at	D43642	0.00482	0.006347	0.0005	0.305805	TCFL1
37056 at	D29767	0.00482	0.006347	0.003934	-0.09702	TEC
31481 s at	M92383	0.00482	0.006347	0.001466	0.219769	TMSB10
35813 at	AA192359	0.00482	0.006347	0.00028	0.17619	TRN-SR
33842 at	AC004472	0.00482	0.006347	0.002169	-0.15115	
41841 at	AF052138	0.00482	0.006347	0.000189	0.441167	
31997 at	X15674	0.00482	0.006347	0.007899	-0.10738	
39738 at	Z82215	0.00482	0.006347	0.002527	0.153792	
39091 at	AF070523	0.00482	0.006634	0.00037	0.437983	JWA
36198 at	D13641	0.00482	0.006634	0.000776	0.275308	KIAA0016
36142 at	X79204	0.00482	0.006634	0.000182	0.256049	SCA1
40420 at	AB015718	0.00482	0.006634	0.001172	0.202412	STK10
33020 at	AF059575	0.00482	0.006634	0.000563	-0.18074	
37178 at	M74089	0.00482	0.006634	0.00076	0.187888	
37604 at	U44111	0.00482	0.006634	0.003845	0.105361	
40979 at	AJ243310	0.00482	0.006921	0.000945	-0.97643	C14orf3
35806 at	W26854	0.00482	0.006921	0.011098	-0.13774	DKFZP434D156
148 at	U88629	0.00482	0.006921	0.001778	-0.16763	ELL2
31692 at	M59830	0.00482	0.006921	0.000221	-1.12882	HSPA1B

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40127 at	M95929	0.00482	0.006921	0.004606	-0.34536	PMX1
234 s at	M57399	0.00482	0.006921	0.010231	-0.14331	PTN
37382 at	N25117	0.00482	0.006921	0.002068	-0.16335	RPS26
37732 at	AL049940	0.00482	0.006921	0.001149	-0.42489	RYBP
39083 at	U39318	0.00482	0.006921	0.001097	-0.24533	UBE2D3
369 s at	Z29331	0.00482	0.006921	0.000193	-0.15851	UBE2H
233 s at	M55682	0.00482	0.006921	0.010264	-0.10921	
36744 at	S58544	0.00482	0.006921	0.005501	-0.11193	
31893 at	L13687	0.00482	0.007311	0.002185	0.114008	ARL2
39309 at	M88714	0.00482	0.007311	0.002075	0.114833	BDKRB2
32107 at	AL050173	0.00482	0.007311	0.001866	0.128954	C21orf25
35282 r at	M33680	0.00482	0.007311	0.002612	0.134487	CD81
37931 at	X05299	0.00482	0.007311	0.003837	0.171613	CENPB
37021 at	X16832	0.00482	0.007311	0.000578	0.177395	CTSH
37894 at	U83410	0.00482	0.007311	0.005207	0.219569	CUL2
36875 at	AL050018	0.00482	0.007311	0.003938	0.220539	DKFZP564B116
36456 at	AL080063	0.00482	0.007311	0.006562	0.186332	DKFZP564I052
36961 at	AL050286	0.00482	0.007311	0.000767	0.221397	DKFZP586A011
37333 at	X63692	0.00482	0.007311	0.003174	0.172997	DNMT1
39367 at	AA522537	0.00482	0.007311	0.002762	0.113812	ELAC2
35942 at	AI183417	0.00482	0.007311	0.006167	0.101739	GABPB1
38065 at	X62534	0.00482	0.007311	0.000973	0.195089	HMG2
33569 at	D50532	0.00482	0.007311	0.001268	0.159735	HML2
37520 at	AJ006591	0.00482	0.007311	0.001379	0.1682	HSA6591
38547 at	Y00796	0.00482	0.007311	0.000438	0.386166	ITGAL
34235 at	AB018301	0.00482	0.007311	0.008701	0.138344	KIAA0758
37030 at	AB020694	0.00482	0.007311	0.002526	0.205561	KIAA0887
32085 at	AB023198	0.00482	0.007311	0.000409	0.275051	KIAA0981
34212 at	AB028958	0.00482	0.007311	0.001533	0.117614	KIAA1035
37360 at	U66711	0.00482	0.007311	0.006567	0.260368	LY6E
35975 at	L13744	0.00482	0.007311	0.007658	0.19599	MLLT3
36012 at	Y09631	0.00482	0.007311	0.000769	0.309898	PIBF1
35621 at	L77213	0.00482	0.007311	0.001122	0.247214	PMVK
39127 f at	X73478	0.00482	0.007311	0.000681	0.242238	PPP2R4
39243 s at	U94319	0.00482	0.007311	0.000688	0.337656	PSIP2
1043 s at	U27516	0.00482	0.007311	0.000222	0.194938	RAD52
37964 at	W25793	0.00482	0.007311	0.000438	0.258505	RNF3
32330 at	X06617	0.00482	0.007311	0.002581	0.116631	RPS11
34646 at	Z25749	0.00482	0.007311	0.001419	0.123333	RPS7
38648 at	U80760	0.00482	0.007311	0.007371	0.161214	TNRC1
33490 at	L27071	0.00482	0.007311	0.000638	0.372837	TXK
36032 at	AL031427	0.00482	0.007311	0.000541	0.367004	
38511 at	AL109722	0.00482	0.007311	0.00187	0.134304	
35585 at	X15675	0.00482	0.007311	0.011165	0.131908	
37971 at	AL050089	0.00482	0.007852	0.001906	-0.23061	BAZ1A
1274 s at	L22005	0.00482	0.007852	0.002439	-0.22532	CDC34

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37960 at	AB014679	0.00482	0.007852	0.003059	-0.13664	CHST2
36618 g at	X77956	0.00482	0.007852	0.000689	-0.22743	ID1
32534 f at	A1814466	0.00482	0.007852	0.001127	-0.1955	VAMP5
1516 g at	HG4074- HT4344	0.00482	0.007852	0.000964	-0.17461	
38703 at	AF005050	0.00482	0.008059	0.001761	0.230395	DNPEP
925 at	J03909	0.00482	0.008059	0.000125	-0.18353	IFI30
32696 at	X59841	0.00482	0.008059	0.000226	0.265756	PBX3
37774 at	A1819942	0.00482	0.009314	0.002286	0.326115	02-Sep
38470 i at	D86981	0.00482	0.009314	0.003441	0.319525	APPBP2
32825 at	Y10805	0.00482	0.009314	0.002583	0.183496	HRMT1L2
478 g at	U51127	0.00482	0.009314	0.00212	0.282678	IRF5
32437 at	U14970	0.00482	0.009314	0.000561	0.144991	RPS5
33813 at	A1813532	0.00482	0.009314	0.00037	-0.41933	TNFRSF1B
39955 at	Y15228	0.00482	0.010363	0.002026	-0.17032	DLEU2
40982 at	AA926957	0.00482	0.010363	0.000909	-0.22483	FLJ10534
40925 at	AA554945	0.00482	0.010363	0.001827	-0.14301	FLJ10803
34039 at	AJ001383	0.00482	0.010363	0.001968	-0.3226	LY94
40199 at	M97676	0.00482	0.010363	0.010011	-0.16313	MSX1
980 at	AF002020	0.00482	0.010363	0.001278	-0.1736	NPC1
1245 i at	U25975	0.00482	0.010363	0.000764	-0.24651	PAK2
1225 g at	X66363	0.00482	0.010363	0.000837	-0.4179	PCTK1
722 at	D87957	0.00482	0.010363	0.004418	-0.14751	RQCD1
32638 s at	A1610467	0.00482	0.010363	0.000699	-0.17683	SMG1
38621 at	AJ012008	0.00482	0.010363	0.002571	-0.32997	
36131 at	AJ012008	0.00482	0.010363	0.001638	-0.16204	

**Table II: Gene Expression Profile from PBMCs of MS vs. Healthy- Highest Scoring Genes (Bonferroni analysis)**

SEQ ID NO:	Affy metri x ID no:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log FoldChange	Symbol
271	32213 at	AA203527	1.37E-05	1.61E-06	1.18E-07	0.281992	RPP20
272	40615 at	AA780049	7.44E-05	2.35E-05	7.39E-07	0.54912	FLJ21439
273	37348_s_at	AA845349	7.44E-05	0.0001187	7.78E-07	0.457176	TRIP7
274	39388 at	AA902713	2.11E-06	1.99E-06	1.44E-06	0.474378	
243	41386_i_at	AB002344	7.44E-05	5.92E-05	8.48E-07	-1.00068	KIAA0346
154	39797 at	AB002347	2.11E-06	1.33E-07	7.19E-10	0.371731	KIAA0349
244	34661 at	AB002348	1.37E-05	3.86E-06	2.49E-07	0.576346	KIAA0350
155	3225	AB002386	2.11E-06	7.73E-07	5.34E-09	0.586117	EZH1

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	9_at						
184	3626 0 at	AB002448	1.37E-05	5.01E-06	2.45E-07	0.468926	
183	4043 1 at	AB007891	1.37E-05	3.86E-06	3.99E-05	0.196376	KIAA0 431
173	3965 0_s_ at	AB007895	1.37E-05	5.01E-06	9.61E-07	0.186643	KIAA0 435
257	3225 3 at	AB007927	2.11E-06	1.99E-06	2.12E-07	0.323787	RERE
254	3969 1 at	AB007960	2.11E-06	9.54E-07	7.96E-06	0.447772	SH3GL B1
182	3443 5 at	AB008775	0.0003443	0.0003041	1.88E-06	-0.80745	AQP9
194	4124 2 at	AB011004	0.0003443	7.05E-06	1.41E-06	-1.34073	UAP1
186	3278 4 at	AB011108	1.37E-05	5.05E-07	4.39E-07	0.453498	PRP4
258	4143 0 at	AB011113	1.37E-05	7.05E-06	3.74E-07	0.444795	WDR7
187	4107 7 at	AB011115	1.37E-05	5.05E-07	3.39E-07	0.382809	KIAA0 543
188	3213 3 at	AB011161	2.57E-08	4.01E-09	9.64E-11	0.63432	PIP5K1 C
197	3885 4 at	AB014535	1.37E-05	5.05E-07	1.04E-06	0.285282	KIAA0 635
245	3737 5 at	AB014538	0.0003443	4.67E-05	1.98E-06	-0.63923	KIAA0 638
246	3531 7 at	AB014579	1.37E-05	5.01E-06	6.08E-08	0.367966	MGEA 5
251	4161 4 at	AB014608	7.44E-05	9.64E-05	4.59E-06	0.41494	KIAA0 708
214	3776 0 at	AB015019	7.44E-05	7.05E-06	2.75E-07	-0.24515	BAIAP 2
210	3887 3 at	AB018343	1.84E-09	4.16E-10	9.05E-12	0.383078	KIAA0 800
223	4143 1 at	AB023153	2.11E-06	1.33E-07	1.82E-08	0.895842	KIAA0 936
255	3645 8 at	AB023235	7.44E-05	1.61E-06	1.43E-05	0.311216	KIAA1 018
240	3235 0 at	AB026118	0.0013772	0.0001897	4.47E-06	-0.24886	MALT1
235	3855 5 at	AB026436	7.44E-05	1.61E-06	0.000219	-0.7589	DUSP1 0
247	3941 7 at	AB028951	2.64E-07	1.72E-07	8.78E-09	0.543028	KIAA1 028
248	3757 1 at	AB028981	2.11E-06	7.73E-07	5.34E-07	0.282288	KIAA1 058
239	4179 6 at	AB029015	2.64E-07	2.49E-07	5.37E-09	0.695063	PLCE2
256	3686 2 at	AB029038	7.44E-05	1.61E-06	7.62E-05	0.364386	KIAA1 115
167	3997 5 at	AC002400	1.37E-05	3.06E-05	2.28E-06	-0.25834	UBPH

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151	358_ at	AF000545	7.44E-05	5.23E-05	3.48E-06	-0.85393	P2Y10
152	3188 8_s_ at	AF001294	1.37E-05	7.05E-06	1.23E-06	-0.76359	TSSC3
159	3592 6_s_ at	AF004230	2.64E-07	1.72E-07	3.06E-07	0.349166	LILRB 1
153	3827 0 at	AF005043	7.44E-05	5.23E-05	2.70E-06	0.408592	PARG
178	3781 9 at	AF007130	2.11E-06	5.05E-07	2.51E-06	0.391811	LOC54 104
179	3876 4 at	AF007142	0.0003443	0.0004443	3.15E-06	0.678734	
180	3527 3 at	AF007151	1.37E-05	5.05E-07	3.25E-06	0.468343	MMS19 L
156	1857 at	AF010193	7.44E-05	2.35E-05	1.26E-07	-1.4705	MADH 7
176	3607 9 at	AF010309	1.37E-05	5.01E-06	7.36E-07	-0.28533	PIG3
157	4084 3 at	AF012023	7.44E-05	5.92E-05	1.02E-06	0.50623	ICAP- 1A
158	1445 at	AF014958	2.11E-06	4.31E-06	1.05E-07	-0.42152	CCRL2
163	3545 0_s_ at	AF015553	2.11E-06	9.54E-07	2.61E-07	0.61214	GTF2I
170	3167 5_s_ at	AF019083	1.37E-05	5.01E-06	8.34E-07	0.17011	PTENP 1
205	3610 0 at	AF022375	2.64E-07	8.23E-08	1.87E-11	-1.35847	VEGF
165	3141 0 at	AF023614	1.37E-05	1.51E-05	4.79E-07	-0.20744	TACI
166	1953 at	AF024710	8.55E-11	8.55E-11	1.13E-12	-1.95537	VEGF
171	3836 5 at	AF026086	0.0003443	4.67E-05	2.66E-06	0.297942	PEX1
193	3862 8 at	AF029777	1.37E-05	7.05E-06	8.27E-07	0.290159	GCN5L 2
169	3275 6 at	AF030249	1.37E-05	1.61E-06	1.98E-07	0.534547	ECH1
172	3779 4 at	AF035281	2.11E-06	2.48E-06	4.87E-07	0.472445	
175	3834 9 at	AF038564	1.37E-05	1.61E-06	2.05E-07	-0.40446	ITCH
204	4049 8_g_ at	AF040707	2.11E-06	1.99E-06	3.57E-07	0.289845	NPR2L
177	3496 2 at	AF042386	1.37E-05	5.01E-06	0.000107	0.137192	PPIE
200	3359 8_r_a t	AF052160	7.44E-05	1.51E-05	1.67E-06	0.623021	
198	3784	AF054176	2.11E-06	1.33E-07	6.47E-09	-0.58138	C1orf7

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	2_at						
203	4006 0_r_a t	AF054589	0.0003443	2.35E-05	1.98E-06	0.945394	
189	3663 9 at	AF061258	7.44E-05	9.64E-05	1.58E-06	0.622201	LIM
190	4086 9 at	AF067853	1.37E-05	5.01E-06	5.02E-06	0.361707	ADSL
191	4087 0_g at	AF069517	2.11E-06	1.33E-07	4.91E-07	0.399638	RBM6
201	3516 5 at	AF070582	2.64E-07	1.72E-07	3.23E-08	-0.19773	MGC13 033
202	3418 8 at	AF070606	1.37E-05	3.06E-05	1.48E-06	-0.89337	
195	3514 2 at	AF070617	1.37E-05	3.86E-06	3.23E-07	0.323494	
208	4183 1 at	AF077820	2.64E-07	2.19E-08	2.91E-08	0.656852	LRP5
213	3723 3 at	AF079167	2.64E-07	2.49E-07	7.37E-10	-1.93249	OLR1
211	3943 0 at	AF082557	0.0013772	4.67E-05	2.23E-06	0.226994	TNKS
215	3956 2 at	AF094481	1.37E-05	5.01E-06	2.74E-07	-0.29045	CGGBP 1
209	3147 2_s at	AF098641	2.64E-07	1.72E-07	1.56E-07	-0.41172	
216	3381 0 at	AF110377	1.37E-05	5.01E-06	3.05E-05	0.361232	TRRAP
252	4138 4 at	AF117829	7.44E-05	0.000129	2.61E-06	-0.57516	RIPK2
275	3568 2 at	AI133727	7.44E-05	0.0001187	1.43E-06	0.181464	FLB642 1
276	4017 5 at	AI141670	0.0003443	0.0003041	1.60E-06	-0.2494	CLCN2
277	4067 0 at	AI148772	0.0003443	4.67E-05	4.18E-06	-1.02619	KYNU
278	3793 6 at	AI184802	2.64E-07	2.19E-08	2.67E-09	-0.21576	HPRP4 P
279	3202 1 at	AI560890	2.57E-08	2.83E-08	1.80E-07	0.179028	
280	3472 4 at	AI670100	7.44E-05	2.58E-05	7.70E-07	0.22677	GRLF1
281	3925 7 at	AI754391	1.37E-05	3.86E-06	1.72E-06	-0.27657	KLF12
282	3648 4 at	AI935146	0.0003443	2.35E-05	2.05E-06	-0.46726	GALN T3
283	3585 0 at	AI950382	1.37E-05	1.61E-06	1.63E-07	-0.74128	KIAA0 585
284	3475 1 at	AI970189	0.0003443	2.35E-05	6.16E-07	-0.75934	KIAA0 997
168	3939 2 at	AJ002190	7.44E-05	1.61E-06	2.17E-08	0.33775	GNPAT

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234	3898 8 at	AJ007042	2.64E-07	1.72E-07	2.10E-07	0.170935	WHSC 1
224	4072 3 at	AJ010059	2.11E-06	5.05E-07	2.95E-06	0.2235	SIT
217	3956 1 at	AL008583	2.64E-07	2.19E-08	1.12E-08	0.250082	CBX6
192	3704 3 at	AL021154	0.0003443	4.67E-05	2.19E-06	-0.82935	ID3
222	3433 3 at	AL021707	0.0003443	7.05E-06	4.95E-06	-2.21462	
199	4072 1_g at	AL022398	7.44E-05	1.61E-06	8.09E-08	0.919627	
199	4072 0 at	AL022398	7.44E-05	7.05E-06	1.10E-07	0.79713	DJ434 O14.3
199	3373 4 at	AL022398	7.44E-05	2.58E-05	2.40E-06	0.493166	
218	3718 9 at	AL023553	1.37E-05	1.75E-05	2.51E-06	0.226635	PMM1
220	3267 2 at	AL049387	0.0013772	0.0001897	5.12E-06	0.379296	
221	3602 1 at	AL049409	7.44E-05	1.51E-05	1.10E-06	0.714173	LEF1
230	3368 7 at	AL049782	7.44E-05	2.58E-05	7.66E-07	0.237794	
231	3423 9 at	AL049787	1.37E-05	5.01E-06	7.11E-06	0.311278	
250	4045 6 at	AL049963	0.0003443	4.67E-05	8.36E-07	-0.74421	LOC64 116
226	4133 5 at	AL050084	7.44E-05	1.61E-06	5.26E-05	0.509331	DC8
227	3997 6 at	AL050087	2.11E-06	2.48E-06	1.27E-07	-0.31279	KIAA1 785
228	3829 6 at	AL050196	1.37E-05	5.01E-06	2.00E-05	-0.24688	DKFZP 586D22 23
229	3189 6 at	AL050281	0.0003443	0.0002051	2.85E-06	0.30517	NAG
232	3696 8_s at	AL050353	0.0003443	2.35E-05	4.42E-06	0.179352	OIP2
233	3809 0 at	AL050371	0.0003443	2.35E-05	3.70E-06	0.493288	PISD
236	3571 5 at	AL080071	0.0003443	0.0003041	3.12E-06	0.237367	DKFZP 564M0 82
237	3885 9 at	AL080141	1.37E-05	5.01E-06	2.42E-07	0.330868	SEC31 B-1
238	3203 3 at	AL096780	1.37E-05	5.05E-07	2.13E-06	0.34487	CHKL
285	3319 2_g at	AW051579	1.37E-05	1.61E-06	7.58E-07	0.593476	FLJ105 12
49	3256 7 at	D10704	1.37E-05	1.75E-05	4.69E-07	-0.36791	CHK

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74	4121 5_s_ at	D13891	2.11E-06	2.48E-06	4.57E-05	-0.20577	ID2
75	3741 1 at	D30758	2.11E-06	1.99E-06	1.58E-05	0.27738	CENTB 1
162	3447 6_r_a t	D30783	2.57E-08	2.83E-08	8.95E-10	-1.65011	EREG
107	3852 3_f_a t	D49677	7.44E-05	7.05E-06	4.18E-06	0.198707	U2AF1 RS2
207	3523 4 at	D50406	1.37E-05	3.86E-06	2.65E-05	0.461907	RECK
110	3368 3 at	D50525	0.0003443	4.67E-05	3.02E-06	0.486698	
133	4066 2_g_ at	D78579	1.37E-05	7.05E-06	4.25E-07	-1.65638	NR4A3
133	4066 1 at	D78579	7.44E-05	7.05E-06	9.62E-07	-1.61438	NR4A3
134	3403 4 at	D80011	7.44E-05	1.61E-06	4.20E-07	-0.35073	KIAA0 189
127	4011 3 at	D87119	7.44E-05	2.35E-05	1.80E-06	0.425625	GS3955
127	717_ at	D87119	7.44E-05	5.23E-05	4.62E-06	0.557116	GS3955
135	3503 9 at	D87466	1.37E-05	8.66E-06	1.49E-07	0.466046	KIAA0 276
286	1877 g at	HG1103- HT1103	1.37E-05	1.61E-06	1.16E-07	-0.39165	
287	1743 s at	HG2007- HT2056	7.44E-05	9.64E-05	4.01E-06	-0.41408	
288	1842 at	HG2724- HT2820	1.37E-05	3.06E-05	5.17E-06	-1.33814	
289	1162 g at	HG3227- HT3404	2.64E-07	1.72E-07	1.68E-08	-0.25361	
290	706_ at	HG4582- HT4987	7.44E-05	2.35E-05	4.63E-07	-0.39588	
30	3802 9 at	J02939	7.44E-05	1.61E-06	2.16E-07	-0.87844	SLC3A 2
63	3380 3 at	J02973	1.37E-05	5.05E-07	2.93E-07	-1.30804	THBD
66	1388 g at	J03258	0.0003443	0.0001695	1.21E-06	-0.58295	VDR
24	3667 4 at	J04130	0.0003443	2.35E-05	3.02E-06	-0.62071	SCYA4
58	3905 7 at	L04733	0.0013772	2.35E-05	8.84E-07	0.306455	KNS2
59	1125 s at	L05424	2.11E-06	1.33E-07	2.27E-09	-0.58081	CD44
99	2061 at	L12002	7.44E-05	4.67E-05	1.23E-06	0.286717	ITGA4
55	280_ g at	L13740	2.64E-07	2.19E-08	5.83E-08	-1.45891	NR4A1
55	279	L13740	1.37E-05	5.01E-06	9.10E-08	-0.61928	NR4A1



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	at						
57	3903 7 at	L13773	1.37E-05	1.75E-05	6.44E-07	0.247919	MLLT2
54	3749 7 at	L16499	1.37E-05	8.66E-06	5.12E-06	0.374296	HHEX
79	3394 3 at	L20941	2.64E-07	1.33E-07	1.78E-06	-0.58618	FTH1
70	1139 at	L22075	2.64E-07	2.49E-07	1.10E-08	-0.55736	GNA13
68	3237 2 at	L22569	1.37E-05	8.66E-06	1.52E-06	0.318129	CTSB
96	3790 3 at	L25665	0.0003443	0.0001695	3.34E-06	-0.4513	GNL1
90	1603 g at	L33881	2.64E-07	1.72E-07	5.06E-08	-0.59585	PRKCI
109	3631 2 at	L40377	1.37E-05	5.05E-07	3.49E-07	-0.79409	SERPI NB8
105	3757 9 at	L47738	2.57E-08	4.01E-09	7.54E-09	0.31646	PIR121
148	1846 at	L78132	7.44E-05	5.23E-05	5.15E-07	0.358576	LGALS 8
46	3663 6 at	M12267	0.0003443	0.0001695	4.07E-06	-0.3279	OAT
60	1106 s at	M12959	7.44E-05	2.58E-05	1.61E-06	0.128482	TRA@
39	3940 2 at	M15330	8.55E-11	8.55E-11	2.49E-12	-2.13825	IL1B
25	3537 2_r_a t	M17017	7.44E-05	0.0001187	1.43E-06	-1.74073	IL8
44	3399 3 at	M22919	2.64E-07	3.12E-07	9.52E-08	-0.81053	MYL6
35	3979 1 at	M23114	2.11E-06	4.31E-06	1.59E-07	-0.96141	ATP2A 2
43	3460 9_g_ at	M24194	7.44E-05	1.61E-06	4.38E-06	0.560895	GNB2L 1
36	3264 0 at	M24283	0.0003443	4.67E-05	3.71E-06	-1.32611	ICAM1
85	3668 0 at	M24895	2.11E-06	1.33E-07	1.72E-08	0.476779	AMY2 B
37	875_ g at	M26683	7.44E-05	0.0001187	3.70E-06	-0.16179	SCYA2
40	1368 at	M27492	0.0003443	0.0004017	2.01E-06	-0.32619	IL1R1
41	1369 s at	M28130	7.44E-05	4.67E-05	8.02E-07	-2.27292	IL8
64	1372 at	M31165	7.44E-05	5.23E-05	1.38E-06	-0.34617	TNFAI P6
61	1373 at	M31523	1.37E-05	1.75E-05	2.09E-06	0.36898	TCF3
33	3402 2 at	M36821	1.37E-05	8.66E-06	2.21E-07	-0.36334	GRO3
62	3840 4 at	M55153	7.44E-05	2.58E-05	4.77E-06	-0.27465	TGM2

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45	1378 g at	M58603	7.44E-05	5.23E-05	1.28E-06	-0.73537	NFKB1
26	2036 s at	M59040	0.0013772	2.35E-05	2.82E-06	-0.46271	CD44
65	4084 2 at	M60784	7.44E-05	5.23E-05	1.24E-06	0.559903	SNRPA
95	3218 1 at	M60922	7.44E-05	1.51E-05	4.47E-08	0.39657	FLOT2
38	1737 s at	M62403	7.44E-05	5.23E-05	5.57E-07	-0.53749	IGFBP 4
27	3619 0 at	M63256	0.0003443	5.92E-05	6.54E-07	0.454561	CDR2
31	4036 5 at	M63904	2.57E-08	1.03E-08	5.38E-09	-0.59612	GNA15
67	3610 1_s_ at	M63978	0.0003443	4.67E-05	1.77E-06	-0.44762	VEGF
42	242_ at	M64571	1.84E-09	1.84E-09	2.41E-11	0.416659	MAP4
91	3832 6 at	M69199	2.11E-06	1.99E-06	1.45E-07	-1.9021	G0S2
48	1252 at	M73547	1.37E-05	5.01E-06	9.20E-08	0.438897	D5S346
34	1231 at	M74525	2.11E-06	2.48E-06	3.50E-07	-0.61792	UBE2B
28	3218 6 at	M80244	0.0003443	7.05E-06	2.72E-06	-0.8522	SLC7A 5
32	3782 5 at	M84443	1.37E-05	5.05E-07	4.08E-07	0.303567	GALK2
29	3979 9 at	M94856	7.44E-05	5.23E-05	4.99E-06	-0.23847	FABP5
47	210_ at	M95678	0.0003443	7.05E-06	2.00E-06	0.432923	PLCB2
241	4142 5 at	M98833	7.44E-05	1.61E-06	1.52E-06	0.434288	FLI1
261	3596 9 at	N23137	2.11E-06	2.48E-06	2.06E-07	0.247311	MPHO SPH9
261	3597 0_g_ at	N23137	0.0013772	0.0001695	4.12E-06	0.244083	MPHO SPH9
262	4088 5_s_ at	N30151	7.44E-05	1.61E-06	5.05E-05	0.393521	STX16
263	4056 4 at	N42007	2.11E-06	2.48E-06	9.19E-05	0.167986	NUP50
264	3969 3 at	N53547	7.44E-05	8.56E-05	1.80E-07	0.296678	MGC55 08
269	3271 5 at	N90862	1.37E-05	5.05E-07	3.28E-08	0.43576	VAMP 8
270	3421 0 at	N90866	2.64E-07	8.23E-08	2.76E-08	0.304525	CDW52
265	3955 1 at	N98667	1.37E-05	8.66E-06	3.38E-07	0.367127	KIAA1 696
260	3477 9 at	R90942	1.37E-05	5.01E-06	1.05E-05	-0.17696	ST6GA LNACI

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							V
53	3296 2 at	S52028	2.11E-06	5.05E-07	9.62E-08	-0.81662	CTH
87	3206 6_g_ at	S68134	0.0003443	7.05E-06	8.37E-07	-1.64652	CREM
87	3206 5 at	S68134	0.0003443	7.05E-06	4.35E-06	-2.47105	CREM
86	3206 7 at	S68271	0.0003443	7.05E-06	3.03E-06	-2.07185	CREM
92	3150 8 at	S73591	1.37E-05	1.51E-05	4.68E-06	0.414777	VDUP1
50	545_ g at	S76638	7.44E-05	2.35E-05	7.47E-07	-0.35416	NFKB2
51	1347 at	S78187	7.44E-05	1.61E-06	1.95E-05	0.203265	CDC25 B
52	3620 9 at	S78771	0.0003443	5.92E-05	2.55E-06	-0.31389	BRD2
126	1237 at	S81914	0.0003443	7.05E-06	4.18E-07	-1.59146	IER3
69	3384 9 at	U02020	1.37E-05	8.66E-06	1.37E-06	-1.13863	PBEF
71	553_ g at	U02570	1.37E-05	2.81E-05	1.26E-06	0.432431	ARHG API
73	554_ at	U03634	1.37E-05	1.75E-05	1.00E-06	-0.21467	LBC
76	1069 at	U04636	0.0003443	5.92E-05	2.81E-06	-1.85123	PTGS2
83	1796 s at	U05681	7.44E-05	5.23E-05	3.37E-06	-0.35383	BCL3
81	1635 at	U07563	7.44E-05	2.35E-05	4.91E-07	-0.25016	ABL1
82	189_ s at	U09937	1.84E-09	4.16E-10	2.04E-09	-1.21578	PLAUR
77	3973 4 at	U10117	7.44E-05	1.51E-05	4.07E-06	0.563673	SCYE1
80	3849 1 at	U11732	1.37E-05	3.86E-06	3.04E-07	-0.22574	ETV6
101	4065 9 at	U12767	7.44E-05	1.61E-06	2.84E-07	-1.23483	NR4A3
101	190_ at	U12767	0.0003443	7.05E-06	2.55E-07	-2.13744	NR4A3
84	525_ g at	U13695	7.44E-05	1.61E-06	1.11E-05	0.805607	PMS1
88	3793 8 at	U15552	1.37E-05	5.01E-06	1.67E-05	-0.68094	HSU15 552
94	3692 9 at	U17760	0.0003443	7.05E-06	4.25E-06	-0.84472	LAMB 3
131	1243 at	U18300	7.44E-05	0.000129	2.43E-06	0.183171	DDB2
93	3978 1 at	U20982	2.11E-06	1.99E-06	1.20E-08	-0.67125	IGFBP 4
104	3345 6 at	U24166	7.44E-05	1.61E-06	7.52E-06	-0.45293	MAPR E1

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121	3770 6 at	U28811	0.0003443	7.05E-06	1.33E-06	0.32855	GLG1
97	493_ at	U29171	1.37E-05	5.01E-06	1.10E-06	-0.6032	CSNK1 D
98	3257 9 at	U29175	1.37E-05	8.66E-06	1.90E-06	0.266342	SMAR CA4
181	3615 9_s_ at	U29185	2.11E-06	7.73E-07	1.56E-07	-1.08006	PRNP
100	3842 9 at	U29344	2.11E-06	9.54E-07	2.35E-07	-0.43842	FASN
106	198_ g at	U29656	2.11E-06	7.73E-07	7.52E-08	0.353186	NME3
106	197_ at	U29656	7.44E-05	0.000129	4.31E-06	0.471876	NME3
102	496_ s at	U32324	1.37E-05	5.05E-07	3.21E-08	0.334966	IL11RA
103	3351 3 at	U33017	2.64E-07	1.72E-07	5.20E-07	0.373581	SLAM
112	3977 9 at	U38847	7.44E-05	2.35E-05	9.91E-07	0.222946	TARBP 1
111	3891 1 at	U41815	1.37E-05	5.05E-07	2.16E-07	-0.96931	NUP98
124	3886 8 at	U43774	0.0003443	2.35E-05	8.80E-07	-0.39938	FCAR
118	162_ at	U44839	2.11E-06	9.54E-07	2.54E-07	-0.97008	USP11
120	3772 3 at	U47414	2.11E-06	9.54E-07	2.31E-06	0.370736	CCNG2
113	3440 5 at	U47927	2.57E-08	2.83E-08	5.53E-09	0.545592	USP5
115	1788 s at	U48807	1.37E-05	5.01E-06	4.97E-08	-0.93178	DUSP4
119	3297 7 at	U49187	7.44E-05	1.51E-05	1.48E-06	0.671467	C6orf32
119	3297 8_g_ at	U49187	7.44E-05	9.64E-05	3.53E-06	0.511392	C6orf32
114	3722 9 at	U49844	7.44E-05	7.05E-06	3.67E-07	0.47168	ATR
130	1527 s at	U50527	1.37E-05	5.01E-06	5.11E-06	0.416543	
122	3812 0 at	U50928	7.44E-05	1.61E-06	4.72E-06	0.302213	PKD2
116	3974 9 at	U51007	7.44E-05	1.51E-05	1.49E-06	0.309996	PSMD4
138	3253 9 at	U51205	1.37E-05	5.05E-07	2.65E-07	-0.76279	COP9
129	3256 3 at	U51478	7.44E-05	2.35E-05	6.10E-07	-0.58	ATP1B 3
117	3606 0 at	U51920	2.11E-06	1.33E-07	7.01E-08	-0.28142	SRP54
128	3435 6 at	U52960	2.11E-06	1.61E-06	1.51E-07	-0.84863	SURB7
125	806	U56998	0.0003443	7.05E-06	3.70E-06	-0.74294	CNK

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	at						
141	4038 5 at	U64197	1.84E-09	1.84E-09	2.95E-10	-0.62373	SCYA2 0
132	1789 at	U65928	7.44E-05	4.67E-05	2.85E-07	0.408918	COPSS
164	3210 5_f_a t	U66063	2.11E-06	2.48E-06	4.70E-07	0.277185	CAMK 2G
161	4013 8 at	U70735	1.37E-05	8.66E-06	1.82E-06	0.249185	MOV34 -34KD
139	3522 7 at	U72066	2.57E-08	1.03E-08	4.33E-08	-0.34482	RBBP8
136	3193 5_s_ at	U75968	2.11E-06	1.99E-06	4.36E-06	0.139542	DDX11
137	4028 9 at	U78107	8.55E-11	3.69E-11	4.04E-12	-0.43769	NAPG
174	3810 4 at	U78302	2.64E-07	1.72E-07	2.41E-08	0.329878	DECR1
140	1209 at	U78798	2.57E-08	4.01E-09	1.11E-06	-0.3172	TRAF6
142	3825 2_s_ at	U84007	7.44E-05	1.61E-06	0.000235	0.236422	AGL
143	3574 1 at	U85245	7.44E-05	1.61E-06	4.57E-07	0.365266	PIP5K2 B
150	4060 6 at	U88629	0.0003443	4.67E-05	9.58E-07	-0.32607	ELL2
147	4132 3 at	U90917	1.37E-05	1.61E-06	3.89E-07	0.433406	FOXM 1
196	3470 7 at	U91543	2.64E-07	3.12E-07	2.01E-07	0.478678	CHD3
149	3827 6 at	U91616	1.37E-05	5.05E-07	1.27E-07	-0.80419	NFKBI E
160	3530 3 at	U96876	7.44E-05	1.61E-06	3.54E-06	-0.45317	INSIG1
185	4060 7 at	U97105	1.37E-05	1.75E-05	6.56E-07	1.00615	DPYSL 2
266	3929 6 at	W28319	1.37E-05	5.01E-06	1.50E-05	0.294631	FBLN1
267	3332 8 at	W28612	1.37E-05	5.01E-06	1.70E-06	-0.25519	
268	3685 6 at	W28743	0.0003443	7.05E-06	2.78E-06	-0.28926	PP1628
18	430_ at	X00737	2.11E-06	9.54E-07	5.21E-08	-0.67074	NP
12	4148 5 at	X02152	1.37E-05	5.05E-07	4.63E-08	-0.75601	LDHA
4	3390 8 at	X04366	1.37E-05	2.81E-05	5.11E-06	0.346076	CAPN1
10	1520 s at	X04500	2.64E-07	1.72E-07	3.43E-10	-2.12121	IL1B
6	3975 3 at	X06256	1.37E-05	2.35E-05	4.89E-07	-0.7357	ITGA5

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16	4089 6 at	X13403	7.44E-05	5.92E-05	4.21E-07	0.146032	POU2F 1
21	1866 g at	X15217	7.44E-05	4.67E-05	3.77E-07	-0.2371	SKIL
20	4149 9 at	X15218	8.55E-11	8.55E-11	1.40E-10	-1.41501	SKI
14	4007 4 at	X16396	0.0003443	0.0002051	3.27E-06	-0.6151	MTHF D2
7	4026 8 at	X16706	7.44E-05	1.61E-06	1.23E-06	-1.09747	FOSL2
11	4126 6 at	X53586	1.37E-05	8.66E-06	3.40E-07	0.51291	ITGA6
1	3214 5 at	X58141	7.44E-05	9.64E-05	1.75E-06	0.384254	ADD1
3	3729 4 at	X61123	7.44E-05	0.0001057	4.17E-07	-1.15256	BTG1
13	4036 2 at	X61498	7.44E-05	1.61E-06	8.80E-07	-0.49884	NFKB2
5	3271 6 at	X62535	1.37E-05	1.61E-06	5.68E-07	0.243937	DGKA
249	3736 5 at	X63368	2.11E-06	5.05E-07	2.30E-08	-0.55432	DNAJB 2
2	4088 1 at	X64330	7.44E-05	7.05E-06	2.27E-06	0.297851	ACLY
22	3918 3 at	X66363	2.64E-07	1.72E-07	6.53E-07	-0.24505	PCTK1
9	3790 4_s_ at	X66436	0.0003443	8.56E-05	1.88E-06	-0.26662	
15	424_ s at	X66945	7.44E-05	1.51E-05	1.91E-07	-0.35494	FGFR1
23	1983 at	X68452	2.57E-08	4.01E-09	9.12E-11	-0.26618	CCND2
19	3244 4 at	X69392	2.64E-07	1.33E-07	1.10E-08	0.297444	RPL26
212	382_ at	X70218	1.37E-05	3.06E-05	2.44E-06	-0.74691	PPP4C
72	4116 9 at	X74039	1.84E-09	4.16E-10	1.51E-10	-0.67381	PLAUR
242	3806 4 at	X79882	1.37E-05	5.05E-07	1.78E-07	0.520965	MVP
89	3846 6 at	X82153	7.44E-05	1.61E-06	2.27E-06	0.47844	CTSK
253	3728 3 at	X82209	2.11E-06	5.05E-07	1.37E-09	-0.45281	MN1
108	3661 4 at	X87949	7.44E-05	1.61E-06	4.05E-07	-0.54468	HSPA5
123	3377 4 at	X98172	7.44E-05	4.67E-05	5.29E-07	0.507556	CASP8
146	3232 9 at	X99142	1.37E-05	8.66E-06	1.24E-06	-0.29773	KRTH B6
144	3915 9 at	X99656	1.37E-05	5.05E-07	1.68E-06	-0.23553	SH3GL 1
17	3718 5 at	Y00630	2.57E-08	3.70E-08	6.65E-09	-2.38485	SERPI NB2

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145	3593 6_g_ at	Y08683	1.37E-05	5.05E-07	4.71E-06	0.492738	CPT1B
206	4072 9_s_ at	Y14768	1.37E-05	5.05E-07	7.26E-08	0.248383	LTB
219	3851 8 at	Y18004	1.37E-05	5.01E-06	4.19E-07	-0.9465	SCML2
8	3753 6 at	Z11697	1.37E-05	5.05E-07	3.55E-06	-1.21033	CD83
56	3568 5 at	Z14000	0.0003443	0.0002051	3.91E-06	-0.33734	RING1
78	3485 7 at	Z24724	2.64E-07	2.19E-08	5.96E-09	-1.10426	
259	3358 8 at	Z32860	1.37E-05	5.01E-06	7.81E-06	0.133192	
225	3975 6_g_ at	Z93930	2.64E-07	2.49E-07	2.42E-05	-0.39839	XBP1

Table III: Differential Gene Expression in acute MS relapse vs. remission

Affy metri x ID no:	Identifier	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Symbol
3859 2_s_ at	AI828210	5.38E-06	5.38E-06	8.37E-06	-0.18947	KIAA0284
4009 6 at	D14710	6.73E-05	3.19E-05	2.89E-05	-0.35496	ATP5A1
3581 6 at	U46692	6.73E-05	3.19E-05	0.000284	-0.49741	CSTB
3331 8 at	AF061261	6.73E-05	3.19E-05	3.22E-05	-0.28274	MBLL
3969 8 at	U51712	6.73E-05	3.19E-05	0.003464	-0.42775	SMAP31
3585 2 at	AB014558	6.73E-05	4.25E-05	0.000473	0.694784	CRY2
4145 8 at	AB007936	6.73E-05	4.25E-05	0.000958	-0.25409	KIAA0467
3488 0 at	AC002115	6.73E-05	4.25E-05	0.000147	0.622841	MGC10433
3496 2 at	AF052160	6.73E-05	4.25E-05	0.000182	-0.46468	
855_ at	S78085	0.000538	0.000104	0.000102	-0.55064	PDCD2
3883 9 at	AL096719	0.000538	0.000104	0.000089	-0.22287	PFN2
3617 6 at	U61234	0.000538	0.000104	0.000844	0.299182	TBCC
3739 1 at	X12451	0.000538	0.000251	0.000876	1.04444	CTSL
4033 7 at	M35531	0.000538	0.000251	0.000241	-0.20303	FUT1

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1457 at	M64174	0.000538	0.000251	3.43E-05	-0.5508	JAK1
4142 3 at	AB018269	0.000538	0.000251	7.39E-05	-0.18186	KIAA0726
3613 0_f_ at	R92331	0.000538	0.000251	0.000104	0.289994	MT1E
828_ at	U19487	0.000538	0.000251	0.001738	-0.25888	PTGER2
3984 7 at	AF040965	0.000538	0.000251	0.000775	0.48898	RES4-25
3297 4 at	U07563	0.000538	0.000251	3.61E-05	-0.16779	RRP4
3631 2 at	L40377	0.000538	0.000251	0.009479	0.452416	SERPINB8
3807 0 at	AL080234	0.000538	0.000251	0.000377	-0.52631	
3547 9 at	AJ242015	0.003096	0.00039	0.013957	0.281618	ADAM28
3931 7 at	D86324	0.003096	0.00039	0.001801	-0.34728	CMAH
3319 5 at	M94065	0.003096	0.00039	0.002391	-0.13976	DHODH
3481 0 at	AC004382	0.003096	0.00039	0.000121	-0.20383	DKFZP434K046
3530 0 at	X54326	0.003096	0.00039	0.002734	-0.39559	EPRS
4043 3 at	W25921	0.003096	0.00039	9.41E-05	-0.39027	GNS
3501 0 at	X92110	0.003096	0.00039	0.000103	-1.00581	HCGVIII-1
4091 3 at	W28589	0.003096	0.00039	0.000225	-0.20949	HSPD1
3341 1_g_ at	S66213	0.003096	0.00039	0.000134	-0.28606	ITGA6
3723 2 at	AB011158	0.000538	0.00039	0.000047	-0.163	KIAA0586
4119 1 at	AB023209	0.003096	0.00039	0.003354	-0.09151	KIAA0992
4003 6 at	AF035940	0.003096	0.00039	0.008457	0.282437	MAGOH
588_ at	M31724	0.003096	0.00039	0.000671	0.569343	PTPN1
1318 at	X74262	0.003096	0.00039	0.000062	-0.37623	RBBP4
1119 at	J05249	0.003096	0.00039	0.00045	-0.52346	RPA2
3436 2 at	M55531	0.003096	0.00039	0.023054	-0.22329	SLC2A5
3514 9 at	AI865431	0.003096	0.00039	0.00027	0.423067	TNFRSF5
3137 2 at	W28203	0.003096	0.00039	0.007983	-0.17484	
3403	W28667	0.003096	0.00039	0.000846	-0.49488	



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6_at						
3931 5 at	D13628	0.000538	0.000529	0.034335	-0.10398	ANGPT1
3701 2 at	U03271	0.000538	0.000529	0.000286	-0.1675	CAPZB
3801 7 at	U05259	0.000538	0.000529	0.003589	0.551328	CD79A
3790 2 at	L13278	0.000538	0.000529	7.27E-05	-0.43636	CRYZ
4061 9 at	M91670	0.000538	0.000529	0.003472	0.600255	E2-EPF
3896 1 at	AB029030	0.000538	0.000529	0.000657	-0.13458	KIAA1107
4130 4 at	AF016098	0.000538	0.000529	0.000433	-0.16189	NRP2
3504 7 at	X76091	0.000538	0.000529	0.004691	0.161349	RFX2
3758 3 at	U52191	0.000538	0.000529	0.00229	1.2356	SMCY
4112 1 at	AA203345	0.000538	0.000529	0.001228	-0.50409	STX16
784_ g at	U96113	0.000538	0.000529	0.000394	-0.41425	WWP1
3165 6 at	AL050263	0.000538	0.000529	0.000224	-0.15981	
4079 8_s_ at	Z48579	0.000538	0.000799	0.000184	-0.30836	ADAM10
4110 9 at	M31452	0.000538	0.000799	0.002899	-0.13022	C4BPA
4016 2_s_ at	AC003107	0.000538	0.000799	0.000262	-0.16818	COMP
893_ at	M91670	0.000538	0.000799	0.000792	0.41925	E2-EPF
3645 8 at	AB023235	0.000538	0.000799	0.001348	-0.30138	KIAA1018
3743 6 at	X89960	0.000538	0.000799	0.026837	-0.35169	MCSP
3660 8 at	D55654	0.000538	0.000799	0.019331	-0.2254	MDH1
3856 9 at	U02683	0.000538	0.000799	0.030035	-0.09324	NRF1
858_ at	S90469	0.000538	0.000799	0.000785	0.23032	POR
3810 8 at	AF020543	0.000538	0.000799	0.004286	-0.25061	PPT2
3621 5 at	M34181	0.000538	0.000799	0.000055	-0.5883	PRKACB
3373 0 at	AF095448	0.000538	0.000799	0.000588	-0.24961	RAI3
4136 3 at	AF027150	0.000538	0.000799	0.000979	-0.16012	SIP1
3367 8 i a	X02344	0.000538	0.000799	0.000918	0.430531	TUBB2

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t						
3367 9_f_ at	X02344	0.000538	0.000799	0.002225	0.296682	TUBB2
3766 2 at	AI701164	0.000538	0.000799	0.000115	-0.23639	UBE2G1
783_ at	U96113	0.000538	0.000799	9.77E-05	-0.45711	WWP1
3330 6 at	AF016052	0.000538	0.000799	0.001254	-0.19092	ZNF24
3820 1 at	U21551	0.003096	0.00103	0.000836	0.278219	BCAT1
1920 s at	X77794	0.003096	0.00103	3.72E-05	-0.81938	CCNG1
3523 0 at	AF070530	0.003096	0.00103	0.014908	0.276942	CL24751
3204 5 at	AB002331	0.003096	0.00103	0.001714	-0.17304	DATF1
3673 2 at	AI004207	0.003096	0.00103	0.000762	-0.1648	FLJ00002
905_ at	L76200	0.003096	0.00103	0.000824	0.444479	GUK1
3350 8 at	U26398	0.003096	0.00103	0.001182	-0.29185	INPP4A
3820 3 at	U69883	0.003096	0.00103	0.007922	0.103614	KCNN1
3737 7_i_a t	M13452	0.003096	0.00103	0.000467	0.405856	LMNA
4128 9 at	AA126505	0.003096	0.00103	0.002	-0.39781	NCAM1
3833 5 at	U88620	0.003096	0.00103	0.007562	-0.3532	OGG1
227_ g at	M33336	0.003096	0.00103	0.001568	-0.26454	PRKAR1A
3787 6 at	AB015982	0.003096	0.00103	0.000382	-0.27486	PRKCN
4144 6_f_ at	H68340	0.003096	0.00103	0.001222	0.516352	RNAHP
3437 5 at	M28225	0.003096	0.00103	0.000686	1.0733	SCYA2
3909 9 at	X97064	0.003096	0.00103	0.003207	-0.19906	SEC23A
4157 3 at	X68560	0.003096	0.00103	0.007856	0.437567	SP3
3778 9 at	AF064094	0.003096	0.00103	0.000287	-0.19385	TADA2L
4161 2 at	AB007872	0.003096	0.00103	0.000119	-0.20778	ZNF264
4098 4 at	W28255	0.013622	0.001698	0.001407	-0.24426	76P
3870 4 at	AB007934	0.003096	0.001698	0.003182	-0.24405	ACF7

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3479 2 at	AL049954	0.013622	0.001698	0.024193	-0.25818	AHCYL1
3876 0_f_ at	U90546	0.003096	0.001698	0.000105	-0.34074	BTN3A2
3871 2 at	AL035291	0.013622	0.001698	0.007668	0.506107	CH1
3534 9 at	AF031647	0.013622	0.001698	0.004755	0.257244	COPS3
3237 0 at	M57888	0.003096	0.001698	0.004549	-0.64384	CTLA1
4009 7 at	AF000987	0.003096	0.001698	0.009455	0.247586	EIF1AY
4025 0 at	U55766	0.003096	0.001698	0.00066	0.795017	HRB2
2061 at	L12002	0.013622	0.001698	0.005765	-0.1942	ITGA4
4163 5 at	D14661	0.013622	0.001698	0.011324	0.391267	KIAA0105
4084 4 at	D63875	0.013622	0.001698	0.002192	-0.36411	KIAA0155
3478 6 at	AB018285	0.013622	0.001698	0.001545	0.550994	KIAA0742
3721 6 at	AB023180	0.013622	0.001698	0.001642	0.253479	KIAA0963
3217 1 at	AL080102	0.013622	0.001698	0.003651	0.435751	KIAA1856
3997 1 at	M22637	0.013622	0.001698	0.003792	-0.27794	LYL1
1764 s at	D85131	0.013622	0.001698	0.005126	-0.12291	MAZ
1761 at	D37965	0.013622	0.001698	0.01111	-0.09143	PDGFRL
3936 4_s_ at	Y18207	0.003096	0.001698	0.003474	-0.17238	PPP1R3C
1571 f at	L49229	0.013622	0.001698	0.000336	-0.36639	RB1
4104 0 at	U77664	0.013622	0.001698	0.002354	0.193666	RPP38
4180 7 at	AL040137	0.003096	0.001698	0.008384	-0.23366	SAP18
3765 4 at	D31764	0.013622	0.001698	0.01295	-0.13299	SNX17
4107 1 at	X57655	0.013622	0.001698	0.002476	-0.17382	SPINK2
3679 0 at	M19267	0.013622	0.001698	0.013582	0.262886	TPM1
1106 s at	M12959	0.013622	0.001698	0.003907	-0.08942	TRA@
3384 4 at	AA160724	0.013622	0.001698	0.005695	0.267002	
3310 3_s_ at	U37122	0.003096	0.002135	0.000571	-0.59281	ADD3

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3855 4 at	AA903720	0.003096	0.002135	0.002557	0.244618	BAP29
3721 1 at	M93107	0.003096	0.002135	0.00187	-0.19146	BDH
4169 4 at	M17754	0.003096	0.002135	0.010333	-0.10769	BN51T
3480 2 at	X15882	0.003096	0.002135	0.0023	0.227769	COL6A2
3841 3 at	D15057	0.003096	0.002135	0.002814	-0.26776	DAD1
3942 0 at	S62138	0.003096	0.002135	0.002442	1.1158	DDIT3
3855 5 at	AB026436	0.003096	0.002135	0.011189	0.711919	DUSP10
3822 6 at	W27152	0.003096	0.002135	0.009498	-0.1614	FLJ10569
763 at	AB001106	0.003096	0.002135	0.002408	0.444617	GMFB
3432 2_r_ at	D87120	0.003096	0.002135	0.00475	0.236706	GS3786
3415 7_f_ at	AI200373	0.003096	0.002135	0.003822	-0.31066	H2AFI
4160 9 at	U15085	0.003096	0.002135	0.011743	0.328857	HLA-DMB
3573 7 at	U90549	0.003096	0.002135	0.001654	-0.26437	HMG17L3
4105 8_g_ at	AI760162	0.003096	0.002135	0.001313	-0.47775	HT012
3483 2_s_ at	AB018306	0.003096	0.002135	0.000371	0.316202	KIAA0763
3901 9 at	D14696	0.003096	0.002135	0.016949	0.259239	LAPTM4A
3323 8 at	U23852	0.003096	0.002135	0.001207	-0.2593	LCK
4013 8 at	U70735	0.003096	0.002135	0.0002	-0.20846	MOV34-34KD
3981 2 at	X79865	0.003096	0.002135	0.0141	0.418466	MRPL12
3908 1 at	AI547258	0.003096	0.002135	0.001223	0.267951	MT2A
269 at	L40387	0.003096	0.002135	0.00038	0.211973	OASL
3437 6 at	AB019517	0.003096	0.002135	0.023004	0.219453	PKIG
4121 4 at	M58459	0.003096	0.002135	0.001362	1.46854	RPS4Y
3332 2_i_a t	X57348	0.003096	0.002135	0.004255	0.22047	SFN
3276 7 at	M74558	0.003096	0.002135	0.001205	0.219185	SIL

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3938 7 at	U34044	0.003096	0.002135	0.000831	-0.21289	SPS
3563 4 at	U49928	0.003096	0.002135	0.000886	-0.31189	TAB1
1634 s at	X05839	0.003096	0.002135	0.008747	0.214552	TGFB1
3746 0 at	U16296	0.003096	0.002135	0.006585	-0.14857	TIAM1
4144 3 at	U63127	0.003096	0.002135	0.000538	-0.38925	TIC
3154 0 at	U03397	0.003096	0.002135	0.005156	-0.34157	TNFRSF9
1110 at	M21624	0.003096	0.002135	0.001748	-0.51878	TRD@
3617 0 at	D83198	0.003096	0.002135	0.028975	-0.17519	YF13H12
303_ at	HG960- HT960	0.003096	0.002135	0.003089	0.145701	
918_ at	HG4724- HT5166	0.003096	0.002135	0.002446	-0.25728	
1197 at	D00654	0.003096	0.004342	9.79E-05	-0.1819	ACTG2
4078 9 at	U54645	0.013622	0.004342	0.004228	-0.25281	AK2
3267 6 at	M93405	0.003096	0.004342	0.020651	0.126156	ALDH6A1
3379 6 at	U73960	0.003096	0.004342	0.002279	0.555806	ARL4
2000 at	U26455	0.003096	0.004342	0.006562	-0.53911	ATM
3383 8 at	M33519	0.003096	0.004342	0.011169	-0.33327	BAT3
4054 8 at	U90028	0.003096	0.004342	0.000396	-0.24971	BICD1
3711 2 at	AB002384	0.003096	0.004342	0.002855	-0.46941	C6orf32
4106 0 at	M74093	0.003096	0.004342	0.000763	-0.33022	CCNE1
4182 1 at	AA203246	0.003096	0.004342	0.007014	-0.16607	CDC2L5
795_ s at	X66358	0.013622	0.004342	0.007122	-0.1886	CDKL1
3730 2 at	U30872	0.003096	0.004342	0.001715	-0.164	CENPF
3715 5 at	AB020675	0.013622	0.004342	0.002913	-0.25056	CNTNAP2
1400 at	M13207	0.013622	0.004342	0.01388	0.122241	CSF2
3434 0 at	AA173896	0.013622	0.004342	0.008401	0.305133	CYB5-M
3549 0 at	L78267	0.003096	0.004342	0.04708	0.103949	D15S226E
3607 8 at	AL080120	0.013622	0.004342	0.001834	-0.12922	DKFZP564O0423

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4006 5_s_ at	U13896	0.013622	0.004342	0.020482	-0.10291	DLG1
3151 4 at	AF034970	0.013622	0.004342	0.010371	-0.10568	DOK2
1306 at	D12686	0.013622	0.004342	0.003493	0.170378	EIF4G1
3225 9 at	AB002386	0.003096	0.004342	0.000131	-0.39255	EZH1
3496 0_g_ at	M15059	0.003096	0.004342	0.002497	0.2061	FCER2
3836 2 at	W27545	0.013622	0.004342	0.004445	0.379682	FLJ20259
3782 5 at	M84443	0.003096	0.004342	0.000101	-0.27085	GALK2
3862 8 at	AF029777	0.013622	0.004342	0.001427	-0.22426	GCN5L2
3795 9 at	D63876	0.013622	0.004342	0.002737	0.396946	GGA3
3471 9 at	AB020645	0.003096	0.004342	0.003907	-0.37377	GLS
466_ at	U77948	0.003096	0.004342	0.000818	-0.35677	GTF2I
4077 8 at	AF035555	0.003096	0.004342	0.018388	-0.17666	HADH2
3973 3 at	AF055001	0.003096	0.004342	0.010744	0.724714	HERPUD1
4123 7 at	D32129	0.003096	0.004342	0.005364	-0.13287	HLA-A
3146 0_f_ at	AF043586	0.003096	0.004342	0.001047	-0.30021	IGL@
3641 2_s_ at	U53831	0.013622	0.004342	0.01853	0.488267	IRF7
4138 7_r_ at	AB002344	0.003096	0.004342	0.001658	0.705775	KIAA0346
4022 2_s_ at	AI677689	0.013622	0.004342	0.004375	-0.1411	KIAA0685
4143 1 at	AB023153	0.003096	0.004342	0.04282	-0.39134	KIAA0936
3891 9 at	AB023226	0.003096	0.004342	0.000111	-0.71413	KIAA1009
4067 0 at	AI148772	0.013622	0.004342	0.03739	0.532454	KYNU
3536 7 at	AB006780	0.003096	0.004342	0.010236	0.178362	LGALS3
3652 7 at	AL050405	0.003096	0.004342	0.008144	0.311843	LOC51634
1671 s at	L35253	0.013622	0.004342	0.001324	-0.46397	MAPK14
3959	R93527	0.013622	0.004342	0.000372	0.264207	MT1H

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4_f_ at						
4163 7 at	AF108145	0.003096	0.004342	0.001206	-0.14877	MYLE
3218 8 at	M96980	0.013622	0.004342	0.002106	-0.16409	MYT1
545_ g at	S76638	0.013622	0.004342	0.04529	0.171344	NFKB2
3336 7_s_ at	D88674	0.013622	0.004342	0.045232	0.346415	OAZIN
3696 8_s_ at	AL050353	0.013622	0.004342	0.016071	-0.11979	OIP2
4044 0 at	AL080119	0.003096	0.004342	0.001961	-0.40821	PAI-RBP1
3485 5 at	X76770	0.013622	0.004342	0.005011	-0.10613	PAPOLA
3999 3 at	D11466	0.003096	0.004342	0.009752	0.738127	PIGA
3536 1 at	W28299	0.003096	0.004342	0.001225	-0.17755	PINK1
3702 8 at	U83981	0.003096	0.004342	0.014327	0.28747	PPP1R15A
116_ at	X14968	0.013622	0.004342	0.004727	0.105215	PRKAR2A
1267 at	M55284	0.003096	0.004342	0.003435	-0.17401	PRKCH
3575 2_s_ at	M15036	0.003096	0.004342	0.010965	-0.25119	PROS1
4051 9 at	Y00638	0.003096	0.004342	0.004977	-0.30956	PTPRC
3620 4 at	Y00815	0.003096	0.004342	0.015344	0.116938	PTPRF
1587 at	M38258	0.003096	0.004342	0.009252	-0.14193	RARG
3520 2 at	AF025654	0.003096	0.004342	0.002302	-0.39122	RNGTT
3794 6 at	M60724	0.013622	0.004342	0.004732	-0.22065	RPS6KB1
4046 7 at	AB006202	0.013622	0.004342	0.003028	-0.18268	SDHD
4159 8 at	AA890010	0.003096	0.004342	0.00546	-0.21285	SEC22L1
4135 2 at	X62822	0.003096	0.004342	0.039707	-0.21593	SIAT1
3364 9 at	L41680	0.003096	0.004342	0.001771	-0.16486	SIAT8D
1866 g at	X15217	0.003096	0.004342	0.007377	0.149306	SKIL
3326 0 at	L13857	0.003096	0.004342	0.005721	-0.11073	SOS1
1031 at	U09564	0.003096	0.004342	0.001203	-0.27717	SRPK1

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3924 6 at	Z75330	0.013622	0.004342	0.031796	-0.11359	STAG1
3727 8 at	X92762	0.003096	0.004342	0.001021	-0.27946	TAZ
3174 2 at	AF064090	0.003096	0.004342	0.006206	0.303013	TNFSF14
471 f at	U47634	0.003096	0.004342	0.0057	0.278205	TUBB4
3349 0 at	L27071	0.003096	0.004342	0.000732	-0.39906	TXK
1423 at	D78514	0.003096	0.004342	0.000681	-0.2599	UBE2G1
3637 8 at	AF085807	0.003096	0.004342	0.005801	0.124457	UPK1A
3208 6 at	U66561	0.003096	0.004342	0.002542	0.448044	ZNF184
3454 4 at	X78925	0.013622	0.004342	0.001898	0.351929	ZNF267
1921 at	HG2510- HT2606	0.013622	0.004342	0.007016	0.179499	
3656 4 at	W27419	0.003096	0.004342	0.006325	0.341787	
3784 2 at	AF054589	0.003096	0.004342	0.030568	-0.50762	
3910 3_s_ at	H98552	0.003096	0.004342	0.017185	-0.1057	
4019 4 at	AI056697	0.003096	0.004342	0.000329	-0.20147	
AFF X- HSA C07/ X003 51_ M st	X00351	0.003096	0.005207	0.001506	-0.12928	ACTB
3573 3 at	AF006082	0.003096	0.005207	0.002797	-0.34587	ACTR2
3922 5 at	Y09443	0.003096	0.005207	0.002286	-0.17646	AGPS
3399 l_g_ at	U22961	0.003096	0.005207	0.003092	0.147932	ALB
3617 2_s_ at	AF002163	0.003096	0.005207	0.002447	-0.37588	AP3D1
3621 l at	D87461	0.003096	0.005207	0.004809	-0.26338	BCL2L2
3734 5 at	AF013759	0.003096	0.005207	0.004946	-0.18574	CALU
1273 r at	L22005	0.003096	0.005207	0.006442	0.131869	CDC34
3467 3_r_ at	AL109689	0.003096	0.005207	0.013291	-0.24945	CGI-142



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3470 7 at	U91543	0.003096	0.005207	0.014143	-0.25258	CHD3
3846 6 at	X82153	0.003096	0.005207	0.013882	-0.31742	CTSK
3677 7 at	AJ001687	0.003096	0.005207	0.000224	-0.64837	D12S2489E
3183 5 at	M13149	0.003096	0.005207	0.008717	-0.13824	HRG
3767 9 at	Y10313	0.003096	0.005207	0.006846	0.464769	IFRD1
3328 1 at	D63485	0.003096	0.005207	0.000985	-0.31599	IKKE
3889 2 at	D87077	0.003096	0.005207	0.043072	-0.21138	KIAA0240
3714 6 at	AB007864	0.003096	0.005207	0.001569	0.256672	KIAA0404
1439 s at	X75346	0.003096	0.005207	0.001841	0.331699	MAPKAPK2
654 at	L07648	0.003096	0.005207	0.010594	0.226817	MXI1
4034 4 at	AB028993	0.003096	0.005207	0.0247	0.133216	NLGN1
3943 5 at	D45333	0.003096	0.005207	0.002104	0.302454	PFDN1
1094 g at	M65254	0.003096	0.005207	0.002619	0.262897	PPP2R1B
3326 5 at	M86852	0.003096	0.005207	0.004274	0.172251	PXMP3
967 g at	X97795	0.003096	0.005207	0.021131	-0.18349	RAD54L
3243 7 at	U14970	0.003096	0.005207	0.001894	-0.1353	RPS5
3691 6 at	X74570	0.003096	0.005207	0.00345	0.210049	SIAT4C
3953 7 at	X98248	0.003096	0.005207	0.010403	-0.50617	SORT1
1640 at	U17714	0.003096	0.005207	0.002081	-0.19372	ST13
3398 9_f_ at	W28869	0.003096	0.005207	0.001369	-0.38498	TEGT
3231 4_g_ at	M12125	0.003096	0.005207	0.000178	-0.09929	TPM2
1600 at	L27071	0.003096	0.005207	0.003834	-0.36074	TXK
1947 g at	M60614	0.003096	0.005207	0.001757	-0.25283	WIT-1
1515 at	HG4074- HT4344	0.003096	0.005207	0.004175	0.589048	
3689 4 at	AL031846	0.003096	0.005207	0.004012	-0.42132	
956 at	HG1980- HT2023	0.003096	0.005207	0.002314	0.711234	
3438	AF022853	0.047678	0.006683	0.002056	-0.30792	ABCC1

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4_at						
4165 4 at	X02994	0.047678	0.006683	0.036598	-0.12393	ADA
3754 3 at	D25304	0.047678	0.006683	0.002258	-0.44746	ARHGEF6
3979 0 at	M23115	0.047678	0.006683	0.016518	-0.1243	ATP2A2
3754 9_g_ at	U87408	0.047678	0.006683	0.008628	-0.33961	B1
3260 6 at	AA135683	0.047678	0.006683	0.010045	0.6329	BASP1
3131 4 at	M22491	0.047678	0.006683	0.020141	-0.10386	BMP3
1096 g at	M28170	0.047678	0.006683	0.014303	0.280093	CD19
4073 8 at	M16336	0.047678	0.006683	0.011755	-0.19993	CD2
1942 s at	U37022	0.047678	0.006683	0.028135	-0.06885	CDK4
450_ g at	U66469	0.047678	0.006683	0.004123	0.616896	CGR19
3984 0 at	AI037867	0.047678	0.006683	0.009634	-0.11973	CKTSF1B1
3149 3_s_ at	J03071	0.047678	0.006683	0.011153	-0.23776	CSH2
594_ s at	M55265	0.047678	0.006683	0.01278	-0.1479	CSNK2A1
1492 f at	M33317	0.047678	0.006683	0.014832	-0.17753	CYP2A7
500_ at	U37143	0.013622	0.006683	0.001908	0.171138	CYP2J2
3786 0 at	AL049942	0.013622	0.006683	0.00076	-0.20245	DKFZP564F1422
4101 8 at	AL050015	0.013622	0.006683	0.008524	-0.13959	DKFZP564O243
4112 4_r_ at	L35594	0.013622	0.006683	0.002806	0.216985	ENPP2
3234 3 at	J03796	0.047678	0.006683	0.002596	-0.28198	EPB41
3599 4 at	AC002398	0.013622	0.006683	0.003226	-0.27062	F25965
3676 2 at	X15376	0.013622	0.006683	0.014388	-0.15607	GABRG2
3185 0 at	M90656	0.047678	0.006683	0.006961	-0.15968	GCLC
4107 4 at	AF062006	0.013622	0.006683	0.001442	0.200117	GPR49
416_ s at	X61755	0.013622	0.006683	0.000491	-0.19331	HOXC5
3476 4 at	D21851	0.047678	0.006683	0.017915	0.153927	KIAA0028

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3636 0 at	AB007976	0.047678	0.006683	0.032427	0.228873	KIAA0507
4111 3 at	AI871396	0.047678	0.006683	0.001957	-0.48312	KIAA0557
3992 4 at	AB020660	0.047678	0.006683	0.001858	-0.27616	KIAA0853
3673 5_f_ at	X93595	0.047678	0.006683	0.026214	0.245064	KIR3DL2
3211 6 at	AB002405	0.047678	0.006683	0.003681	-0.19481	LAK-4P
3861 1 at	X07228	0.047678	0.006683	0.046458	0.113484	LIPC
3445 9 at	U50529	0.047678	0.006683	0.001977	0.310499	LOC88523
3863 9 at	AF040963	0.047678	0.006683	0.012629	0.148739	MAD4
1325 at	U59423	0.047678	0.006683	0.01126	-0.1341	MADH1
4082 3_s_ at	U85430	0.013622	0.006683	0.000224	-0.41454	NFATC3
3913 7 at	X80878	0.047678	0.006683	0.010021	-0.16096	NFRKB
337_ at	AF005043	0.013622	0.006683	0.00078	-0.15296	PARG
3197 9 at	D49818	0.047678	0.006683	0.021976	-0.10631	PFKFB4
3290 4 at	M28393	0.013622	0.006683	0.003241	-0.16419	PRF1
4051 8 at	Y00062	0.047678	0.006683	0.011868	-0.2415	PTPRC
4081 6 at	L07758	0.047678	0.006683	0.008943	0.201883	PWP1
809_ at	U57094	0.047678	0.006683	0.014944	-0.31108	RAB27A
228_ at	M35416	0.013622	0.006683	0.002789	-0.41233	RALB
4157 2_r_ at	X75042	0.047678	0.006683	0.003614	0.659166	REL
4045 7 at	AF038250	0.047678	0.006683	0.004198	0.395171	SFRS3
3749 0 at	L27213	0.013622	0.006683	0.001014	-0.13065	SLC4A3
3217 9_s_ at	Y09568	0.047678	0.006683	0.005799	-0.3407	SNAP23
4015 0 at	AA205857	0.013622	0.006683	0.00048	0.27495	SNRPD3
1029 s at	U07794	0.047678	0.006683	0.007632	-0.20733	TXK
4137 7_f_ at	J05428	0.013622	0.006683	0.00573	-0.08342	UGT2B7

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4171 3 at	U09848	0.047678	0.006683	0.011538	-0.26846	ZNF36
3664 2 at	J00287	0.047678	0.006683	0.000953	-0.28381	
3938 3 at	AB007882	0.013622	0.009369	0.006034	-0.17275	ADCY6
3226 1 at	AF072810	0.013622	0.009369	0.016137	-0.32509	BAZ1B
4079 0 at	AB004066	0.013622	0.009369	0.00789	0.494455	BHLHB2
3657 8 at	U37547	0.013622	0.009369	0.00478	0.544595	BIRC2
3910 9 at	AB024704	0.013622	0.009369	0.010893	-0.11914	C20orf1
3217 7_s_ at	AC004084	0.013622	0.009369	0.005491	-0.17437	CAPRI
3150 6_s_ at	L12691	0.013622	0.009369	0.018291	-0.18848	DEFA3
1272 at	L19161	0.013622	0.009369	0.001645	-0.27253	EIF2S3
4006 7 at	M82882	0.013622	0.009369	0.003966	0.478256	ELF1
3731 8 at	X81625	0.013622	0.009369	0.003918	0.762544	ETF1
3495 9 at	M15059	0.013622	0.009369	0.035106	0.313247	FCER2
4077 2 at	AA284298	0.013622	0.009369	0.028745	-0.12535	FLJ22269
3724 5 at	U13044	0.013622	0.009369	0.017986	-0.32813	GABPA
3626 2 at	Z12173	0.013622	0.009369	0.001297	-0.32703	GNS
3982 3 at	U06631	0.013622	0.009369	0.003506	-0.37935	H326
3866 1 at	X75315	0.013622	0.009369	0.002959	1.06191	HSRNASEB
4177 5 at	AF064084	0.013622	0.009369	0.017927	-0.10308	ICMT
3803 0 at	AB002330	0.013622	0.009369	0.048512	-0.09076	KIAA0332
4178 8_i_a t	AB014569	0.013622	0.009369	0.010011	0.709572	KIAA0669
3475 1 at	AI970189	0.013622	0.009369	0.001778	0.569801	KIAA0997
4082 9 at	AB028960	0.013622	0.009369	0.001825	-0.15403	KIAA1037
3777 8 at	AJ005273	0.013622	0.009369	0.001449	0.379277	KIN
3285 5 at	L00352	0.013622	0.009369	0.004231	0.554465	LDLR
3344 7 at	X54304	0.013622	0.009369	0.000863	-0.19567	MLCB

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4062 6_at	AI693193	0.013622	0.009369	0.023978	-0.25831	MTX1
3300 2_at	AF047487	0.013622	0.009369	0.001312	-0.33746	NCK2
4012 2_at	AF037448	0.013622	0.009369	0.00743	0.204106	NSAP1
4120 2_s_ at	AF000152	0.013622	0.009369	0.025216	-0.34592	OS4
3852 6_at	U02882	0.013622	0.009369	0.017536	0.892321	PDE4D
392_ g_at	X89416	0.013622	0.009369	0.005129	-0.1405	PPP5C
1043 s_at	U27516	0.013622	0.009369	0.004164	-0.17553	RAD52
3348 5_at	D23660	0.013622	0.009369	0.01215	0.149327	RPL4
3342 l_s_ at	AB016247	0.013622	0.009369	0.019879	0.416634	SC5DL
3548 8_at	U44754	0.013622	0.009369	0.005273	0.158396	SNAPC1
4187 l_at	AI660929	0.013622	0.009369	0.000698	-0.15764	T1A-2
3732 4_at	X01060	0.013622	0.009369	0.005079	0.27369	TFRC
3380 3_at	J02973	0.013622	0.009369	0.006825	0.835338	THBD
1729 at	L41690	0.013622	0.009369	0.020209	-0.32814	TRADD
3912 3_s_ at	X89066	0.013622	0.009369	0.000396	-0.2226	TRPC1
3440 2_at	AB024327	0.013622	0.009369	0.031	0.260875	UNRIP
3400 l_at	AF033199	0.013622	0.009369	0.02842	-0.1806	ZNF204
3921 8_at	AL080123	0.013622	0.009369	0.018447	0.215445	ZNF23
3976 2_at	AB007885	0.013622	0.009369	0.025803	-0.22701	ZNF262
834_ at	U40462	0.013622	0.009369	0.004101	-0.29722	ZNFN1A1
1146 at	HG3477- HT3670	0.013622	0.009369	0.00042	-0.2367	
253_ g_at	L42324	0.013622	0.009369	0.015195	0.283048	GPR18
3173 6_at	AA975427	0.013622	0.009369	0.002377	-0.26992	
3917 0_at	AL049957	0.013622	0.009369	0.007809	0.133451	
4072 0_at	AL022398	0.013622	0.009369	0.017529	-0.48579	
694_ at	HG2689- HT2785	0.013622	0.009369	0.029818	0.202486	

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4156 5 at	AF034373	0.013622	0.014679	0.00591	-0.26511	A2LP
3703 8 at	X83467	0.013622	0.014679	0.006111	-0.25837	ABCD3
3476 1_r_ at	U41766	0.047678	0.014679	0.014363	0.473526	ADAM9
3310 2 at	D67031	0.013622	0.014679	0.007826	-0.4645	ADD3
3825 3 at	U84011	0.013622	0.014679	0.012995	-0.2499	AGL
1912 s at	M74088	0.013622	0.014679	0.038601	-0.16952	APC
1863 s at	U67092	0.047678	0.014679	0.047381	-0.10935	ATM
3866 3 at	AI033692	0.047678	0.014679	0.010056	-0.2417	BCRP1
394_ at	X92106	0.013622	0.014679	0.001377	-0.33994	BLMH
3956 5 at	Z22535	0.047678	0.014679	0.021613	-0.09832	BMPR1A
3874 0 at	X79067	0.047678	0.014679	0.0381	0.14954	BRF1
3386 4 at	X86098	0.013622	0.014679	0.000807	-0.34829	BS69
3663 4 at	U72649	0.047678	0.014679	0.029157	0.227444	BTG2
3978 2 at	X95592	0.047678	0.014679	0.014127	0.201273	C1D
3203 1 at	D78586	0.047678	0.014679	0.028845	-0.05709	CAD
1421 at	D30742	0.047678	0.014679	0.028215	0.180381	CAMK4
3185 4 at	AF035582	0.047678	0.014679	0.002042	0.530946	CASK
487_ g at	U60521	0.047678	0.014679	0.002353	0.552837	CASP9
3700 9 at	AL035079	0.013622	0.014679	0.00063	-0.78567	CAT
3956 2 at	AF094481	0.047678	0.014679	0.024569	0.149973	CGGBP1
3420 0 at	X83378	0.013622	0.014679	0.025603	0.133485	CLCN6
3608 0 at	AB002332	0.047678	0.014679	0.003136	-0.20009	CLOCK
3976 8 at	D13146	0.013622	0.014679	0.017967	-0.13385	CNP
3595 5 at	S80864	0.013622	0.014679	0.011106	-0.33164	CYCL
3798 1 at	D17530	0.047678	0.014679	0.005519	-0.15234	DBN1
3918 2 at	U87947	0.047678	0.014679	0.011279	0.222382	EMP3
3798 6 at	M60459	0.047678	0.014679	0.010174	-0.10156	EPOR

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3273 l at	AB018247	0.013622	0.014679	0.000348	0.423577	FE65L2
3218 7 at	AB028973	0.013622	0.014679	0.046458	-0.12088	FLJ10883
4140 6 at	AL080172	0.047678	0.014679	0.02693	-0.063	FLJ21919
3474 0 at	AF032886	0.047678	0.014679	0.009814	0.232307	FOXO3A
3918 l at	U00928	0.047678	0.014679	0.01307	-0.0915	FUS
909_ g at	M14660	0.047678	0.014679	0.011038	0.732462	FUT10
3648 4 at	AI935146	0.047678	0.014679	0.044653	0.246267	GALNT3
3770 6 at	U28811	0.047678	0.014679	0.007572	-0.21558	GLG1
3543 5_s_ at	AF001903	0.013622	0.014679	0.001957	-0.28636	HADHSC
102_ at	Y09306	0.047678	0.014679	0.045083	-0.08024	HIPK3
4036 9_f_ at	AL022723	0.047678	0.014679	0.041021	0.165267	HLA-G
3501 7_f_ at	M80469	0.013622	0.014679	0.037453	-0.12099	HLA-J
3761 8 at	M16937	0.013622	0.014679	0.002262	-0.13536	HOXB7
3154 l at	X98307	0.013622	0.014679	0.011852	-0.0908	HSUR7SEQ
1179 at	HG2855- HT2995	0.047678	0.014679	0.030595	0.16813	HSP70
3661 4 at	X87949	0.047678	0.014679	0.028569	0.296273	HSPA5
3273 6 at	W68830	0.013622	0.014679	0.007971	-0.22855	HSPC022
1185 at	D49410	0.047678	0.014679	0.040369	0.153358	HUMIL3RA12
3581 5 at	AL049470	0.013622	0.014679	0.010492	0.283688	HYPB
3579 7 at	Y10659	0.047678	0.014679	0.024205	-0.1217	IL13RA1
3760 3 at	X52015	0.047678	0.014679	0.006637	0.417081	IL1RN
3553 9 at	AF047492	0.047678	0.014679	0.002557	0.25738	IMPG1
3350 7_g_ at	U96919	0.013622	0.014679	0.003221	-0.19947	INPP4A
3607 4 at	U12897	0.013622	0.014679	0.002496	-0.15016	IPW
4104 9 at	S62539	0.013622	0.014679	0.012982	-0.20615	IRS1
3213	AF029778	0.047678	0.014679	0.018006	-0.14486	JAG2

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7_at						
3336 3 at	W25934	0.047678	0.014679	0.016925	0.363279	JTV1
1612 s at	X56681	0.047678	0.014679	0.004935	0.713663	JUND
3819 7 at	M64934	0.047678	0.014679	0.003162	-0.1823	KEL
3484 4 at	D86975	0.047678	0.014679	0.048475	0.163408	KIAA0222
3198 2 at	AB020701	0.013622	0.014679	0.013946	0.283086	KIAA0894
3587 8 at	AB023141	0.047678	0.014679	0.017326	-0.33543	KIAA0924
3273 5 at	AB023148	0.013622	0.014679	0.016218	-0.27496	KIAA0931
3471 2 at	AB023227	0.047678	0.014679	0.043542	0.316063	KIAA1010
3269 3 at	AB028963	0.047678	0.014679	0.039194	-0.12296	KIAA1040
3785 7 at	AL080188	0.047678	0.014679	0.016745	-0.10387	KIAA1775
3671 7 at	AJ224162	0.013622	0.014679	0.002225	-0.24337	LAS
288 s at	L25931	0.013622	0.014679	0.00482	-0.2367	LBR
3542 6 at	AC004410	0.047678	0.014679	0.017457	0.210096	LOC56928
3181 5_r_ at	AB009462	0.047678	0.014679	0.012892	0.131673	LRP3
4183 1 at	AF077820	0.013622	0.014679	0.003095	-0.40005	LRP5
3844 1_s_ at	X59408	0.047678	0.014679	0.018321	-0.3029	MCP
3903 7 at	L13773	0.013622	0.014679	0.002741	-0.18297	MLLT2
3728 3 at	X82209	0.047678	0.014679	0.010828	0.178564	MN1
3514 5 at	X96401	0.013622	0.014679	0.001643	0.317165	MNT
879 at	M30818	0.047678	0.014679	0.032832	0.292682	MX2
3772 4 at	V00568	0.013622	0.014679	0.008535	-0.58978	MYC
1904 at	D50692	0.013622	0.014679	0.043374	-0.20783	MYCBP
3725 0 at	AB007191	0.013622	0.014679	0.022026	-0.18098	MYCBP
989 at	X17576	0.013622	0.014679	0.001641	-0.26027	NCK1
4036 2 at	X61498	0.013622	0.014679	0.006234	0.307667	NFKB2
3916 1 at	AF052093	0.047678	0.014679	0.001318	-0.31976	NJMU-R1



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430_ at	X00737	0.047678	0.014679	0.037385	0.219194	NP
3384 9 at	U02020	0.047678	0.014679	0.014866	0.650286	PBEF
1223 at	X66362	0.047678	0.014679	0.006159	0.137944	PCTK3
3836 5 at	AF026086	0.047678	0.014679	0.006555	-0.18222	PEX1
1275 at	L25441	0.047678	0.014679	0.011907	0.146471	PGGT1B
4044 6 at	AL021366	0.013622	0.014679	0.002775	0.425217	PHF1
751_ at	D85418	0.013622	0.014679	0.004449	-0.31688	PIGC
353_ at	D30037	0.047678	0.014679	0.001579	-0.21226	PITPNB
3277 5_r_ at	AB006746	0.047678	0.014679	0.0356	0.189986	PLSCR1
3216 7 at	AF054182	0.013622	0.014679	0.002098	-0.54761	PMPCB
857_ at	S87759	0.013622	0.014679	0.007522	0.39052	PPM1A
3163 5_g_ at	M13057	0.047678	0.014679	0.032523	-0.19317	PRH1
3837 1 at	M64992	0.047678	0.014679	0.047326	0.178696	PSMA1
3189 2 at	X58288	0.047678	0.014679	0.002633	0.409542	PTPRM
1753 s at	AD000092	0.047678	0.014679	0.028359	0.137917	RAD23A
3753 0_s_ at	U79716	0.013622	0.014679	0.003409	0.195389	RELN
4170 5 at	U69198	0.047678	0.014679	0.048001	0.085316	RFNG
4138 4 at	AF117829	0.047678	0.014679	0.003668	0.377251	RIPK2
3334 2 at	AF039029	0.047678	0.014679	0.002146	-0.28622	RNUT1
4127 7 at	AW02154 2	0.013622	0.014679	0.000677	-0.29232	SAP18
4038 5 at	U64197	0.047678	0.014679	0.021124	0.220476	SCYA20
3631 6_r_ at	AB023136	0.013622	0.014679	0.00288	-0.10963	SEC15B
3759 7_s_ at	AF055006	0.013622	0.014679	0.011241	0.238955	SEC6
3432 7 at	Z46606	0.047678	0.014679	0.005778	-0.1566	SMARCA3
3326 8 at	L25270	0.047678	0.014679	0.002401	-0.15644	SMCX

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3735 3_g_ at	M60618	0.013622	0.014679	0.006316	0.235838	SP100
3203 8_s_ at	AI739308	0.013622	0.014679	0.001861	-0.57419	SRP46
3435 6 at	U52960	0.047678	0.014679	0.02599	0.429086	SURB7
3755 3 at	D50863	0.013622	0.014679	0.006582	-0.13005	TESK1
4176 2 at	D64015	0.013622	0.014679	0.007587	-0.3629	TIAL1
3830 3 at	AB001523	0.047678	0.014679	0.027565	0.164838	TMEM1
3845 7 at	L21715	0.013622	0.014679	0.000862	0.309808	TNNI2
3194 3_g_ at	AF045583	0.047678	0.014679	0.043887	-0.16757	TULP3
3188 2 at	AJ001340	0.013622	0.014679	0.002396	-0.17031	U3-55K
3482 4 at	AB015344	0.013622	0.014679	0.008107	-0.31161	UBQLN2
3665 3_g_ at	J03824	0.013622	0.014679	0.005864	-0.18849	UROS
3480 3 at	AF022789	0.047678	0.014679	0.006582	0.309267	USP12
1926 at	U48801	0.013622	0.014679	0.003849	-0.17743	VEGFB
1665 s at	HG544- HT544	0.047678	0.014679	0.010549	0.454218	
3161 8 at	S66666	0.013622	0.014679	0.003364	-0.14303	
3281 5 at	AI687419	0.047678	0.014679	0.039394	-0.3657	
3364 8 at	W28800	0.047678	0.014679	0.004582	0.270831	
3475 2 at	AL080111	0.013622	0.014679	0.001378	-0.36029	
3493 9_r_ at	AF070536	0.047678	0.014679	0.006685	0.199364	
3607 1 at	AF070633	0.047678	0.014679	0.010142	-0.1635	
3636 8 at	AF054998	0.013622	0.014679	0.007913	-0.21157	
701_ s at	HG3725- HT3981	0.047678	0.014679	0.027792	-0.11953	
954_ s at	HG1614- HT1614	0.013622	0.014679	0.006999	-0.45233	
3938 5 at	M22324	0.013622	0.01669	0.009982	0.283293	ANPEP
3249 0 at	AC005955	0.013622	0.01669	0.004346	0.137324	CEACAM4

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3206 6_g_ at	S68134	0.013622	0.01669	0.005372	1.92718	CREM
3206 7 at	S68271	0.013622	0.01669	0.009154	1.49785	CREM
3983 9 at	M24069	0.013622	0.01669	0.003022	0.249971	CSDA
3835 5 at	AF000984	0.013622	0.01669	0.004295	0.46432	DBY
3557 1 at	AF055917	0.013622	0.01669	0.015434	0.102855	F2RL3
3628 9_f_ at	U27333	0.013622	0.01669	0.012662	0.136047	FUT6
3270 6 at	X89887	0.013622	0.01669	0.009728	0.152829	HIRA
1568 s at	L42243	0.013622	0.01669	0.002638	0.218644	IFNAR2
3585 0 at	AI950382	0.013622	0.01669	0.00744	0.601631	KIAA0585
3585 1_g_ at	AI950382	0.013622	0.01669	0.002126	0.519735	KIAA0585
3692 9 at	U17760	0.013622	0.01669	0.044392	0.431131	LAMB3
3372 0 at	L48692	0.013622	0.01669	0.041233	0.63409	LOC56902
3740 6 at	X94232	0.013622	0.01669	0.016402	0.326694	MAPRE2
4106 3_g_ at	AA037278	0.013622	0.01669	0.01607	0.119411	MGC10882
280_ g at	L13740	0.013622	0.01669	0.007795	0.355688	NR4A1
4065 9 at	U12767	0.013622	0.01669	0.011648	1.30268	NR4A3
4066 1 at	D78579	0.013622	0.01669	0.005896	1.11766	NR4A3
3222 7 at	X17042	0.013622	0.01669	0.015594	0.239796	PRG1
843_ at	U48296	0.013622	0.01669	0.003124	0.864101	PTP4A1
570_ at	M83221	0.013622	0.01669	0.012321	0.192956	RELB
3804 0 at	AF107463	0.013622	0.01669	0.009662	0.419254	SPF30
904_ s at	L47276	0.013622	0.01669	0.004673	0.194449	TOP2A
429_ f at	X00734	0.013622	0.01669	0.010039	0.347307	TUBB5
4010 3 at	X51521	0.013622	0.01669	0.010303	0.60161	VIL2
3365 8 at	S54641	0.013622	0.01669	0.008483	0.183207	ZNF124
3841	M91029	0.013622	0.022759	0.010686	0.450612	AMPD2

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7_at						
3855 0 at	AB021638	0.136189	0.022759	0.024881	-0.1126	APBA3
3687 2 at	AL120559	0.013622	0.022759	0.004505	0.577915	ARPP-19
3260 7 at	AF039656	0.013622	0.022759	0.006991	0.68481	BASP1
3428 6 at	AB020623	0.047678	0.022759	0.009696	0.418826	BCAS2
4002 3 at	X60201	0.013622	0.022759	0.011758	-0.1576	BDNF
4091 0 at	U56637	0.047678	0.022759	0.008899	-0.28102	CAPZA1
3757 2 at	AW04369 0	0.047678	0.022759	0.031971	0.134862	CCK
3976 7 at	D13627	0.047678	0.022759	0.019298	0.203913	CCT8
806_ at	U56998	0.013622	0.022759	0.024403	0.442545	CNK
3282 0 at	U71267	0.047678	0.022759	0.007233	-0.13426	CNOT4
3866 0 at	F27891	0.047678	0.022759	0.02847	0.119514	COX6A2
3657 3 at	U78524	0.013622	0.022759	0.002554	0.353034	DDXBP1
4049 4 at	AF043733	0.047678	0.022759	0.005645	0.22771	DEDD
3899 2 at	X64229	0.013622	0.022759	0.013033	-0.20244	DEK
3415 1 at	AL050284	0.047678	0.022759	0.002819	0.232244	DKFZP586M101 9
4122 6 at	L05147	0.013622	0.022759	0.021168	0.111752	DUSP3
1639 -s at	U15642	0.013622	0.022759	0.013339	0.474421	E2F5
4127 5 at	U31556	0.047678	0.022759	0.011303	0.335871	E2F5
3196 5 at	AC004262	0.047678	0.022759	0.004968	-0.25642	EMR2
3597 2 at	AA181196	0.047678	0.022759	0.009459	-0.10534	FLJ11712
3471 5 at	U74612	0.013622	0.022759	0.014802	-0.18783	FOXM1
3578 5 at	W28281	0.013622	0.022759	0.011042	0.813742	GABARAPL1
3594 2 at	AI183417	0.013622	0.022759	0.011016	0.117979	GABPB1
1598 g at	L13720	0.013622	0.022759	0.014471	-0.1601	GAS6
3513 0 at	X15722	0.013622	0.022759	0.029451	-0.19175	GSR
4137 1 at	Y07595	0.013622	0.022759	0.003113	-0.20996	GTF2H4
3757	L43821	0.047678	0.022759	0.005863	-0.20401	HEF1

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4_at						
3312 3 at	L10379	0.013622	0.022759	0.02006	-0.15961	HRIHFB2206
3934 8 at	X99209	0.013622	0.022759	0.021333	-0.14942	HRMT1L1
3661 7 at	X77956	0.013622	0.022759	0.009598	0.591031	ID1
3433 3 at	AL021707	0.013622	0.022759	0.004161	1.79061	KIAA0063
3898 4 at	AB007896	0.013622	0.022759	0.006273	-0.41247	KIAA0436
3995 3_i_a t	AB014528	0.047678	0.022759	0.001992	-0.31837	KIAA0628
3240 5 at	AB014607	0.013622	0.022759	0.000764	-0.15753	KIAA0707
3842 4 at	AB018290	0.013622	0.022759	0.034506	-0.28703	KIAA0747
4169 1 at	AB018337	0.013622	0.022759	0.008466	-0.41118	KIAA0794
3708 1 at	AB023161	0.013622	0.022759	0.018461	-0.15095	KIAA0944
4100 1 at	AB023202	0.013622	0.022759	0.005879	-0.19156	KIAA0985
3481 5 at	U80743	0.013622	0.022759	0.000544	-0.30322	KIAA1498
3382 0_g_ at	X13794	0.047678	0.022759	0.018671	-0.12764	LDHB
3839 0 at	Z34975	0.013622	0.022759	0.012256	-0.29089	LDLC
4005 9_r_ at	AI341656	0.047678	0.022759	0.021482	-0.26002	LIM
3563 0 at	X87342	0.013622	0.022759	0.006652	-0.23382	LLGL2
2004 at	U29671	0.047678	0.022759	0.001133	-0.2617	MAP3K1
3477 0 at	Z14138	0.013622	0.022759	0.00408	0.81232	MAP3K8
3533 9 at	AI743606	0.013622	0.022759	0.00269	-0.19764	MEL
3898 7 at	AF052183	0.013622	0.022759	0.002151	-0.19631	MGC2722
3832 5 at	AL050356	0.013622	0.022759	0.002743	-0.42417	MINPP1
4087 8_f_ at	AF041081	0.013622	0.022759	0.019282	-0.21627	MN7
484 at	U59302	0.013622	0.022759	0.003859	0.280175	NCOA1
3904 0 at	W28360	0.013622	0.022759	0.016633	0.272057	NCUBE1
3263 9 at	U97198	0.013622	0.022759	0.001352	-0.20163	NLP_1

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4128 2_s_ at	AA194159	0.013622	0.022759	0.004614	-0.40044	PEX10
178_ f at	U38964	0.013622	0.022759	0.004912	-0.23793	PMS2L8
1875 f at	D38498	0.013622	0.022759	0.003965	-0.58306	PMS2L9
3585 8 at	AA996066	0.013622	0.022759	0.003514	-0.21994	PMS2L9
3345 7 at	AB029028	0.013622	0.022759	0.027753	-0.29778	RAP140
4026 1 at	AA402524	0.047678	0.022759	0.005359	-0.11564	RBM9
3984 1 at	U79745	0.013622	0.022759	0.00409	0.777629	SLC16A6
3511 3 at	X98332	0.013622	0.022759	0.002282	-0.20078	SLC22A1
3207 4 at	D42045	0.013622	0.022759	0.006867	-0.19726	SNM1
3210 8 at	M76231	0.013622	0.022759	0.009942	0.13899	SPR
4059 6 at	U76366	0.013622	0.022759	0.015416	-0.09378	TCOF1
3268 2 at	U09087	0.013622	0.022759	0.00607	-0.26017	TMPO
3775 0 at	AF049140	0.047678	0.022759	0.011115	-0.21894	UBE2V2
3610 2 at	AF038962	0.047678	0.022759	0.007219	-0.44337	VDAC3
3478 1 at	D84145	0.013622	0.022759	0.002923	0.574155	WS-3
4153 2 at	Y09723	0.047678	0.022759	0.001292	0.234149	ZNF151
3292 6 at	AL049991	0.013622	0.022759	0.007094	0.245237	
3564 5 at	AL050148	0.013622	0.022759	0.013128	-0.26398	
3862 3 at	AI014538	0.013622	0.022759	0.003507	-0.15278	
4017 7 at	AI732885	0.047678	0.022759	0.043886	-0.10293	
AFF X- hum _alu_ at	U14573	0.013622	0.022759	0.04259	-0.11614	
1700 at	U82987	0.013622	0.024606	0.00343	-0.17272	BBC3
935_ at	L12168	0.013622	0.024606	0.007944	-0.22028	CAP
4038 2 at	V00571	0.013622	0.024606	0.005873	0.132015	CRH
4071 9 at	AL022398	0.013622	0.024606	0.015005	-0.44535	DJ434O14.3
3579	AL080081	0.013622	0.024606	0.007659	0.548836	DNAJB9

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9_at						
4041 9_at	X85116	0.013622	0.024606	0.039531	-0.24601	EPB72
3758 4_at	AJ007669	0.013622	0.024606	0.019404	-0.23162	FANCG
4117 7_at	AW02428 5	0.013622	0.024606	0.007049	0.311562	FLJ12443
3466 2_at	W27666	0.013622	0.024606	0.009544	-0.25685	FLJ14393
4127 4_at	AA908993	0.013622	0.024606	0.015356	-0.12684	FLJ14393
4132 3_at	U90917	0.013622	0.024606	0.016602	-0.23386	FOXMI
3813 9_at	AF017445	0.013622	0.024606	0.025525	-0.33517	FPGT
3651 5_at	AJ238764	0.013622	0.024606	0.030667	0.197763	GNE
3729 9_at	J04501	0.013622	0.024606	0.007821	-0.23523	GYS1
3232 1_at	X56841	0.013622	0.024606	0.022605	-0.23469	HLA-E
3819 4_s_ at	M63438	0.013622	0.024606	0.005389	-0.75873	IGKC
3341 0_at	S66213	0.013622	0.024606	0.011362	-0.09802	ITGA6
4001 8_at	AB007870	0.013622	0.024606	0.002855	0.657213	KIAA0410
4125 8_at	N29665	0.013622	0.024606	0.008301	-0.49779	KIAA0618
3658 8_at	AB018353	0.013622	0.024606	0.033864	-0.3542	KIAA0810
3243 4_at	D10522	0.013622	0.024606	0.028464	0.22227	MACS
3324 5_at	AF004709	0.013622	0.024606	0.018118	-0.09931	MAPK13
4184 3_r_ at	W28275	0.013622	0.024606	0.005871	-0.27591	MGC11061
3376 9_at	AF087020	0.013622	0.024606	0.032064	-0.13544	MPZL1
1719 at	U61981	0.013622	0.024606	0.012069	-0.20932	MSH3
4057 1_at	U90942	0.013622	0.024606	0.004002	0.179029	MYO5A
743_ at	D50370	0.013622	0.024606	0.008327	-0.11492	NAP1L3
4147 5_at	U91512	0.013622	0.024606	0.00493	0.549889	NINJ1
3973 5_at	AF069987	0.013622	0.024606	0.007336	-0.16953	NIT1
1248 at	U37689	0.013622	0.024606	0.007097	-0.17369	POLR2H
1295 at	L19067	0.013622	0.024606	0.006406	0.148517	RELA

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3758 5 at	X13482	0.013622	0.024606	0.016873	0.241998	SNRPA1
778 s at	D16827	0.013622	0.024606	0.004314	-0.16954	SSTR5
3882 2 at	AB011420	0.013622	0.024606	0.030791	0.171669	STK17A
3500 6 at	L39060	0.013622	0.024606	0.026797	-0.24028	TAF1A
3280 2 at	AB011169	0.013622	0.024606	0.004017	-0.24355	TEB4
1328 at	U69108	0.013622	0.024606	0.024472	-0.17595	TRAF5
4124 2 at	AB011004	0.013622	0.024606	0.00265	1.03158	UAP1
3388 4_s_ at	AB014584	0.013622	0.024606	0.028525	-0.1337	UBE4B
1790 s at	HG3914- HT4184	0.013622	0.024606	0.025854	-0.12454	
3358 8 at	Z32860	0.013622	0.024606	0.002037	-0.11041	
3661 1 at	U25849	0.013622	0.024606	0.00632	-0.43498	
3681 8 at	AF052100	0.013622	0.024606	0.006718	-0.2297	
3738 1_g_ at	X59268	0.013622	0.024606	0.003586	0.479423	GTF2B
3876 4 at	AF007142	0.013622	0.024606	0.01864	-0.34584	
4064 2 at	AI312646	0.013622	0.024606	0.027596	-0.14991	
3793 9 at	AL022318	0.047678	0.028192	0.049355	-0.11704	APOBEC1L
3489 8 at	M30704	0.047678	0.028192	0.00926	0.279668	AREG
3596 8_s_ at	AF001307	0.047678	0.028192	0.018109	-0.12594	ARNT
3646 3 at	AB020680	0.047678	0.028192	0.007009	0.227256	BAG5
3727 4 at	AF018631	0.047678	0.028192	0.008344	-0.13689	BTD
3721 8 at	D64110	0.047678	0.028192	0.022809	0.398412	BTG3
3753 6 at	Z11697	0.047678	0.028192	0.024131	0.750492	CD83
3969 5 at	M31516	0.047678	0.028192	0.021562	0.517068	DAF
3974 4 at	AF000982	0.047678	0.028192	0.025357	0.29808	DDX3
3203 2 at	L77566	0.047678	0.028192	0.01243	0.178957	DGSI
4015 4 at	AL096725	0.047678	0.028192	0.007381	0.436688	DKFZP434B103



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3756 4 at	AL080201	0.047678	0.028192	0.044829	-0.11576	DKFZP434F162
3696 1 at	AL050286	0.047678	0.028192	0.004267	-0.22397	DKFZP586A011
3420 1 at	Y13350	0.047678	0.028192	0.015562	0.137002	DNAJA2
4106 7 at	AJ223333	0.047678	0.028192	0.013836	-0.17437	DNMT2
267_ at	L34075	0.047678	0.028192	0.013848	-0.25236	FRAP1
3433 2 at	D31766	0.047678	0.028192	0.029287	-0.09623	GNPI
3169 3_f_ at	Z80776	0.047678	0.028192	0.002034	0.143491	H2AFG
1122 f at	K03183	0.047678	0.028192	0.040298	0.163306	HUMCGBBA3
1501 at	X57025	0.047678	0.028192	0.009135	0.437394	IGF1
4148 3_s_ at	X56681	0.047678	0.028192	0.012885	0.423181	JUND
4124 3 at	AB007916	0.047678	0.028192	0.00772	-0.45744	KIAA0447
3340 7 at	AI672098	0.047678	0.028192	0.014331	0.160649	KIAA0934
3321 9 at	AB029020	0.047678	0.028192	0.035285	-0.3101	KIAA1097
3916 3 at	W27233	0.047678	0.028192	0.019918	-0.24802	KIDINS220
3513 9 at	AL049341	0.047678	0.028192	0.001943	-0.3086	LOC57209
3729 7 at	AL049422	0.047678	0.028192	0.028823	0.264129	LOC84549
1857 at	AF010193	0.047678	0.028192	0.003729	0.927225	MADH7
4127 9_f_ at	AF007134	0.047678	0.028192	0.009151	-0.1209	MAPK8IP1
1124 at	L04731	0.047678	0.028192	0.025599	-0.07236	MLL
3970 7 at	AB014547	0.047678	0.028192	0.023787	-0.15831	MTMR4
3827 6 at	U91616	0.047678	0.028192	0.018681	0.377931	NFKBIE
3762 3 at	X75918	0.047678	0.028192	0.019713	1.21948	NR4A2
3751 8 at	AL049842	0.047678	0.028192	0.022698	0.201258	NUFIP1
3362 8_g_ at	U57843	0.047678	0.028192	0.011796	-0.13969	PIK3CD
546_ at	S76965	0.047678	0.028192	0.012413	0.426208	PKIA
3718	AL023553	0.047678	0.028192	0.00321	-0.15608	PMM1

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9_at						
1463 at	M93425	0.047678	0.028192	0.019899	-0.36854	PTPN12
3215 6 at	AF044968	0.047678	0.028192	0.006887	0.121898	PVRL2
621 at	M28211	0.047678	0.028192	0.050065	-0.08518	RAB4
3876 2 at	AF083255	0.047678	0.028192	0.021248	-0.27368	RNAHP
3289 9_s_ at	U04897	0.047678	0.028192	0.013893	0.278167	RORA
3265 8 at	AL031228	0.047678	0.028192	0.020491	-0.22382	SACM2L
3699 8_s_ at	Y08262	0.047678	0.028192	0.008184	-0.34195	SCA2
3811 0 at	AF000652	0.047678	0.028192	0.001533	0.415218	SDCBP
3418 9 at	D31891	0.047678	0.028192	0.00536	-0.18144	SETDB1
3588 3 at	X66079	0.047678	0.028192	0.008707	0.129642	SPIB
3220 1 at	Z96932	0.047678	0.028192	0.013622	-0.14003	SSNA1
3387 3 at	D43642	0.047678	0.028192	0.015302	-0.26409	TCFL1
3325 3 at	D50919	0.047678	0.028192	0.016207	-0.23972	TRIM14
4056 7 at	X01703	0.047678	0.028192	0.004339	0.386096	TUBA3
3610 0 at	AF022375	0.047678	0.028192	0.015198	0.503607	VEGF
4154 2 at	AF062346	0.047678	0.028192	0.014763	0.455053	ZNF216
3169 7_s_ at	J04755	0.047678	0.028192	0.014444	0.302274	
3287 8_f_ at	AA524802	0.047678	0.028192	0.036226	-0.24775	
3922 3 at	AL096749	0.047678	0.028192	0.017041	0.106309	
3868 0 at	M21259	0.047678	0.028192	0.025927	0.18378	
3690 2 at	X61587	0.047678	0.037364	0.024028	0.222788	ARHG
3766 1 at	J04027	0.047678	0.037364	0.019918	0.336927	ATP2B1
3317 4_s_ at	W28091	0.047678	0.037364	0.016936	-0.1567	BBS4
2031 s at	U03106	0.047678	0.037364	0.004064	0.915096	CDKN1A

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4014 9 at	AL049924	0.047678	0.037364	0.001517	-0.23208	DKFZP547G1110
3593 4 at	L19161	0.047678	0.037364	0.006578	-0.49859	EIF2S3
3939 0 at	AF052123	0.136189	0.037364	0.013524	-0.24445	FLJ10814
3982 7 at	AA522530	0.047678	0.037364	0.038021	0.413536	FLJ20500
3576 9 at	AJ011001	0.047678	0.037364	0.016436	-0.63045	GPR56
476_ s at	U50079	0.047678	0.037364	0.013178	-0.37546	HDAC1
4021 9 at	AI796944	0.047678	0.037364	0.011597	0.216392	HIS1
4067 4_s_ at	S82986	0.047678	0.037364	0.006441	-0.20652	HOXC6
4112 2 at	AB011173	0.047678	0.037364	0.01376	-0.26283	KIAA0601
3704 1 at	AB023160	0.047678	0.037364	0.029467	-0.23276	KIAA0943
3228 8_r_ at	AJ001685	0.047678	0.037364	0.015208	-0.48906	KLRC3
3353 1 at	AJ000673	0.047678	0.037364	0.009021	-0.38103	KLRD1
3850 0 at	AB002450	0.047678	0.037364	0.003391	-0.37426	LOC51014
3748 6_f_ at	U68385	0.047678	0.037364	0.007651	-0.16327	MEIS3
4054 7 at	AI688516	0.047678	0.037364	0.017859	-0.15146	NDUFA2
3265 1 at	W28770	0.047678	0.037364	0.005269	-0.16121	NP25
3271 9 at	L41827	0.047678	0.037364	0.011308	0.139896	NRG1
4008 8 at	X84373	0.047678	0.037364	0.00725	0.77533	NRIP1
1115 at	M25897	0.047678	0.037364	0.025747	-0.41462	PF4
475_ at	U50062	0.047678	0.037364	0.018154	0.19401	RIPK1
3236 4 at	AJ011785	0.047678	0.037364	0.017907	-0.07616	SIX6
3313 1 at	X70683	0.047678	0.037364	0.0155	-0.10219	SOX4
3179 7 at	AL035699	0.047678	0.037364	0.006561	-0.15185	TBPL1
3343 9 at	D15050	0.047678	0.037364	0.016133	0.990791	TCF8
3236 0_s_ at	AF017146	0.047678	0.037364	0.002975	-0.20652	TOP3B
3785	U54996	0.047678	0.037364	0.00691	-0.17359	ZW10

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4_at						
705_at	HG4234-HT	0.047678	0.037364	0.003258	-0.13985	
1520_s_at	X04500	0.047678	0.058634	0.02228	0.857952	IL1B

**Table IV: Differential Gene Expression in MOG-reactive T-cells- MS vs. Healthy**

Affymetrix ID no:	Identifier	Symbol	Name	Function	Fold Change	Pvalue t-test
1586_at	Up regulated M35878	IGFBP3	insulin-like growth factor binding protein 3	modulate IGF activity	5.8	0.03
39765_at	AB002318	KIAA0320	KIAA0320 protein		2.4	0.05
1953_at	AF024710	VEGF	vascular endothelial growth factor	endothelial cell proliferation	2.3	0.02
38829_r_at	AA628946	KHSRP	KH-type splicing regulatory protein	mRNA processing	2.2	0.01
635_s_at	L42374	PPP2R5B	protein phosphatase 2, regulatory subunit B	protein phosphatase	2.1	0.05
34600_s_at	U54644	TUB	tubby (mouse) homolog	may be a transcription factor	1.8	0.01
33293_at	AB023167	KIAA0950	lifeguard	Apoptosis	1.8	0.006
37003_at	X62654	CD63	CD63 antigen (melanoma 1 antigen)	growth regulation	1.8	0.03
39103_s_at	H98552		cDNA DKFZp586I0523		1.8	0.01
35986_at	AL050395	MOF	member of MYST acetyl transferases	histone acetyl transferases	1.7	0.03
37490_at	L27213	SLC4A3	solute carrier family 4, anion exchange 3	inorganic anion exchanger	1.7	0.01
32246_g_at	AF014837	M6A	putative methyltransferase	Transcription factor	1.6	0.05
31788_at	AB014537	KIAA0637	KIAA0637 gene product	Apoptosis	1.5	0.003
32192_g_at	D13969	ZNF144	zinc finger protein 144 (Mel-18)	DNA-Binding protein	1.5	0.04
34066_at	AJ012590	H6PD	hexose-6-phosphate dehydrogenase	Oxidoreductase	1.5	0.04
2060_at	M13995	BCL2	B-cell CLL/lymphoma 2	Apoptosis	1.5	0.03
36337_at	AI760801		chromosome 19, cosmid R31180		1.5	0.009
40997_at	AI660963	MAP3K12	mitogen-activated protein 3 kinase 12	Transferase cytoplasmic	1.5	0.02
1184_at	Down regulated D45248	PSME2	proteasome activator subunit 2 (PA28 beta)	Protein degradation	-1.5	0.04
33328_at	W28612		ESTs		-1.5	0.02
39105_at	Z46389	VASP	vasodilator-stimulated phosphoprotein	Signal transduction	-1.6	0.02
32222_at	AA152202	FLJ14639	hypothetical protein		-1.6	0.02

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FLJ14639

41460_at	AF080561	RBM14	RNA binding motif protein 14	RNA binding protein	-1.7	0.03
35322_at	D50922	KIAA0132	Kelch-like ECH-associated protein 1	ECH-associated protein 1	-1.7	0.03
37474_at	AF025441	OIP5	Opa-interacting protein 5		-1.8	0.04
31853_at	AF080227	EED	embryonic ectoderm development	transcriptional repressor	-1.8	0.04
722_at	D87957	RQCD1	required for cell differentiation	sex differentiation	-1.9	0.03
40362_at	X61498	NFKB2	nuclear factor of kappa light polypeptide Bcells	expression of inflammatory genes	-1.9	0.05
276_at	X52425	IL4R	interleukin 4 receptor	receptor signalling protein	-2	0.04
404_at	L08069	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	protein folding and transport	-2	0.04
39858_s at	AF071504	STX11	syntaxin 11	protein transport	-2.1	0.03
1104_s at	M11717	HSPA1A	heat shock 70kD protein 1A	heat shock response	-2.2	0.03
31692_at	M59830	HSPA1B	heat shock 70kD protein 1B	heat shock response	-2.2	0.03
258_at	M16441	TNF	Human tumor necrosis factor	Inflammatory response	-2.3	0.05
1427_g at	D89077	SLA	Src-like-adaptor		-2.4	0.05
37306_at	U77949	CDC6	cell division cycle 6, S. cerevisiae homolog	DNA replication checkpoint	-2.5	0.02
1536_at	D38549	KIAA0068	KIAA0068 protein		-2.5	0.01
1670_at	L23959	TFDP1	transcription factor Dp-1	cycle progression G1 to S-phase	-2.5	0.01
626_s at	L78833	BRCA1	Breast cancer susceptibility gene		-2.7	0.04
36879_at	M63193	ECGF1	endothelial cell growth factor 1	stimulates angiogenesis	-2.8	0.01
41657_at	AF035625	STK11	serine/threonine kinase 11	Peutz-Jeghers syndrome	-2.9	0.04
36674_at	J04130	SCYA4	small inducible cytokine A4	Cell-to-cell signalling	-2.9	0.05
32618_at	X93086	BLVRA	biliverdin reductase A	biliverdin reductase	-4	0.03

**Table V: Differential Gene Expression in Probable MS vs. Healthy**

affymetrix ID no:	Identification	TNOM PValue	Info PValue	t-Test PValue	Log Fold Change	Gene Symbol
218290_at	NM_018049.1	0.000233	0.000233	2.46E-05	0.438337	FLJ10297

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203162 s at	NM 005886.1	0.000233	0.000233	0.000553	0.35972	KATNB1
204224 s at	NM 000161.1	0.000233	0.000233	0.000297	-0.48848	GCH1
200881 s at	NM 001539.1	0.000233	0.000233	0.000144	-0.58017	DNAJA1
211699 x at	AF349571.1	0.004202	0.004202	0.000274	1.78925	HBA1
209116 x at	M25079.1	0.004202	0.004202	0.000247	1.59503	HBB
217414 x at	V00489	0.004202	0.004202	0.000268	1.54947	
211745 x at	BC005931.1	0.004202	0.004202	0.000296	1.48707	HBA2
214414 x at	T50399	0.004202	0.004202	0.000275	1.43533	HBA2
219269 at	NM 024567.1	0.004202	0.004202	0.002206	1.42146	FLJ21616
209458 x at	AF105974.1	0.004202	0.004202	0.001086	1.3896	HBA1
204018 x at	NM 000558.2	0.004202	0.004202	0.000707	1.3348	HBA1
213515 x at	AI133353	0.004202	0.004202	0.000897	1.29746	HBG2
217232 x at	AF059180	0.004202	0.004202	0.000309	1.29355	
211696 x at	AF349114.1	0.004202	0.004202	0.000163	1.27511	HBB
217529 at	BE547674	0.004202	0.004202	0.002947	0.636619	
207641 at	NM 012452.1	0.004202	0.004202	0.000541	0.570818	TNFRSF13B
43544 at	AA314406	0.004202	0.001401	0.002013	0.520631	TRAP95
202926 at	NM 015909.1	0.004202	0.001401	0.000398	0.501733	NAG
217763 s at	NM 006868.1	0.004202	0.004202	0.002711	0.49862	RAB31
209790 s at	BC000305.1	0.004202	0.004202	0.006921	0.475733	CASP6
32032 at	L77566	0.004202	0.001401	0.00033	0.446293	DGSI
205396 at	BF971416	0.004202	0.004202	0.002405	0.410742	DKFZP586N072 1
202759 s at	BE879367	0.004202	0.004202	0.00056	0.382484	AKAP2
201284 s at	NM 001640.2	0.004202	0.001401	0.004091	0.36631	APEH
205851 at	BC001808.1	0.004202	0.004202	0.012997	0.347043	NM23-H6
212194 s at	AL049539	0.004202	0.004202	0.010738	0.2822	KIAA0255
222125 s at	BC000580.1	0.004202	0.001401	0.014166	0.270658	PH-4
203274 at	NM 012151.2	0.004202	0.001401	0.000685	0.267664	F8A
217931 at	BC004423.1	0.004202	0.004202	0.012194	0.249144	TNRC5
200053 at	NM 004890.1	0.004202	0.001401	0.010332	0.134439	SPAG7
40612_a t	AB029040	0.004202	0.004202	0.010819	-0.14172	KIAA1117
218107 at	NM 025160.1	0.004202	0.001401	0.004986	-0.21141	FLJ21016
221873 at	AW162015	0.004202	0.004202	0.301224	-0.24766	ZNF143
204249 s at	NM 005574.2	0.004202	0.004202	0.107595	-0.24939	LMO2
200777 s at	NM 014670.1	0.004202	0.004202	0.025534	-0.27225	BZW1
213198 at	AL117643.1	0.004202	0.004202	0.046495	-0.27766	
221761 at	AA628948	0.004202	0.001401	0.000319	-0.28951	ADSS
211686 s at	AF251062.1	0.004202	0.001401	0.000435	-0.30924	LOC84549
212501 at	AL564683	0.004202	0.004202	0.018258	-0.44633	CEBPB
203885 at	NM 014999.1	0.004202	0.004202	0.001021	-0.47304	RAB21
219620 x at	NM 017723.1	0.004202	0.004202	0.02759	-0.49548	FLJ20245
204924 at	NM 003264.1	0.004202	0.004202	0.002592	-0.49551	TLR2
210275 s at	AF062347.1	0.004202	0.004202	0.00529	-0.51432	ZNF216
203927 at	NM 004556.1	0.004202	0.004202	0.001134	-0.53489	NFKBIE
215009 s at	U92014.1	0.004202	0.004202	0.003064	-0.59511	

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204435 at	NM 014778.1	0.004202	0.004202	0.001106	-0.65156	KIAA0410
207108 s at	NM 015384.1	0.004202	0.004202	0.002943	-0.68193	IDN3
215501 s at	AK022513.1	0.004202	0.004202	0.001326	-0.68416	DUSP10
201110 s at	NM 003246.1	0.004202	0.001401	0.000162	-1.44745	THBS1
201109 s at	AI812030	0.004202	0.001401	7.42E-05	-1.51098	THBS1
204848 x at	NM 000559.1	0.035714	0.035247	0.006202	1.93991	HBG1
204419 x at	NM 000184.1	0.035714	0.04225	0.009164	1.67513	HBG2
212531 at	NM 005564.1	0.035714	0.04225	0.010814	1.03322	LCN2
209889 at	AF274863.1	0.035714	0.00747	0.007719	0.952868	SEC31B-1
207509 s at	NM 002288.2	0.035714	0.015406	0.010689	0.834313	LAIR2
211430 s at	M87789.1	0.035714	0.04225	0.058518	0.79032	IGHG3
219630 at	NM 005764.1	0.035714	0.04225	0.053679	0.789147	DD96
216379 x at	AK000168.1	0.035714	0.04225	0.038176	0.763766	KIAA1919
208161 s at	NM 020037.1	0.035714	0.035247	0.061379	0.746143	ABCC3
216576 x at	AF103529.1	0.035714	0.035247	0.015284	0.736268	
215379 x at	AV698647	0.035714	0.035247	0.017411	0.616137	IGLJ3
214739 at	AI357539	0.035714	0.04225	0.00558	0.601843	MGC4126
206468 s at	NM 015935.1	0.035714	0.035247	0.021683	0.593818	CGI-01
37201 at	D38535	0.035714	0.04225	0.016025	0.571168	ITIH4
222056 s at	AA723370	0.035714	0.04225	0.039917	0.570325	LOC51011
209322 s at	AF227968.1	0.035714	0.00747	0.005308	0.566516	SH2B
217418 x at	X12530.1	0.035714	0.04225	0.056335	0.559172	MS4A1
214316 x at	AI348935	0.035714	0.035247	0.014129	0.546773	CALR
204139 x at	NM 003422.1	0.035714	0.04225	0.006737	0.536815	ZNF42
205933 at	NM 015559.1	0.035714	0.04225	0.028795	0.536316	SETBP1
220068 at	NM 013378.1	0.035714	0.035247	0.005191	0.532564	VPREB3
204738 s at	NM 004912.1	0.035714	0.015406	0.003037	0.52082	CCM1
201115 at	NM 006230.1	0.035714	0.015406	0.007471	0.517979	POLD2
205267 at	NM 006235.1	0.035714	0.035247	0.021726	0.515263	POU2AF1
212955 s at	AL037557	0.035714	0.00747	0.002786	0.511724	POLR2I
204377 s at	NM 014703.1	0.035714	0.00747	0.006709	0.4938	KIAA0800
203871 at	NM 015670.1	0.035714	0.035247	0.045708	0.464156	SEN3
213062 at	AA643304	0.035714	0.015406	0.004712	0.459694	
203196 at	AI948503	0.035714	0.04225	0.017964	0.45625	ABCC4
210356 x at	BC002807.1	0.035714	0.04225	0.100759	0.455683	MS4A1
209586 s at	AF123539.1	0.035714	0.035247	0.028286	0.454603	HTCD37
212813 at	AA149644	0.035714	0.00747	0.02413	0.450082	JAM3
210542 s at	BC000585.1	0.035714	0.04225	0.033113	0.44368	SLC21A11
210036 s at	AB044806.1	0.035714	0.04225	0.007766	0.433985	KCNH2
215299 x at	U37025	0.035714	0.035247	0.046971	0.427213	SULT1A1
218440 at	NM 020166.2	0.035714	0.035247	0.006318	0.423798	MCCC1
206066 s at	NM 002876.1	0.035714	0.035247	0.026644	0.414867	RAD51C
206132 at	NM 002387.1	0.035714	0.035247	0.01092	0.409481	MCC
206761 at	NM 005816.1	0.035714	0.04225	0.103051	0.407348	TACTILE
213434 at	H95263	0.035714	0.035247	0.069113	0.406766	
200957 s at	NM 003146.1	0.035714	0.035247	0.003146	0.405309	SSRP1

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204857 at	NM 003550.1	0.035714	0.035247	0.054105	0.403851	MAD1L1
212932 at	AK022494.1	0.035714	0.00747	0.001189	0.397073	RAB3GAP
200932 s at	NM 006400.2	0.035714	0.035247	0.021072	0.396297	DCTN2
202799 at	NM 006012.1	0.035714	0.035247	0.015241	0.394779	CLPP
203488 at	NM 014921.1	0.035714	0.035247	0.014463	0.394308	LEC2
207758 at	NM 025056.1	0.035714	0.00747	0.01912	0.393739	FLJ23185
204442 x at	NM 003573.1	0.035714	0.04225	0.026053	0.393337	LTBP4
205756 s at	NM 000132.2	0.035714	0.035247	0.005292	0.392442	F8
210140 at	AF031824.1	0.035714	0.035247	0.190243	0.389129	CST7
206586 at	NM 001841.1	0.035714	0.035247	0.07115	0.387067	CNR2
220078 at	NM 018391.1	0.035714	0.035247	0.138584	0.386982	FLJ23277
215283 at	U79248.1	0.035714	0.00747	0.007475	0.386419	
221196 x at	NM 024332.1	0.035714	0.04225	0.039154	0.386198	C6.1A
221969 at	BF510692	0.035714	0.04225	0.046782	0.385324	PAX5
49679 s at	AA243774	0.035714	0.035247	0.050456	0.381631	MMP24
206853 s at	AL121964	0.035714	0.035247	0.107681	0.373759	MAP3K7
210580 x at	L25275.1	0.035714	0.035247	0.020684	0.372971	SULT1A3
212314 at	AB018289.1	0.035714	0.035247	0.002286	0.37263	KIAA0746
203709 at	NM 000294.1	0.035714	0.035247	0.011432	0.367693	PHKG2
210386 s at	BC001906.1	0.035714	0.035247	0.107947	0.366899	MTX1
208488 s at	NM 000651.1	0.035714	0.04225	0.047953	0.365471	CR1
202564 x at	NM 001667.1	0.035714	0.00747	0.009661	0.362105	ARL2
213051 at	AI133727	0.035714	0.00747	0.018354	0.358884	ZAP
209177 at	BC002873.1	0.035714	0.035247	0.048711	0.358052	DKFZP564J0123
203677 s at	NM 004178.2	0.035714	0.035247	0.007313	0.356459	TARBP2
201138 s at	BG532929	0.035714	0.035247	0.037215	0.356254	SSB
205541 s at	NM 018094.1	0.035714	0.035247	0.014302	0.351314	GSPT2
40255 at	AC004531	0.035714	0.00747	0.01714	0.350445	DDX28
217887 s at	NM 001981.1	0.035714	0.035247	0.010776	0.347051	EPS15
212960 at	AB020689.1	0.035714	0.035247	0.024594	0.346253	KIAA0882
203615 x at	NM 001055.1	0.035714	0.035247	0.056416	0.344937	SULT1A1
218431 at	NM 022067.1	0.035714	0.035247	0.001332	0.337713	FLJ12707
203309 s at	NM 000195.1	0.035714	0.00747	0.014156	0.3312	HPS1
204617 s at	NM 022914.1	0.035714	0.00747	0.167735	0.331082	24432
204394 at	NM 003627.1	0.035714	0.035247	0.062759	0.330371	POV1
218581 at	NM 022060.1	0.035714	0.035247	0.010717	0.328122	FLJ12816
213581 at	BF446180	0.035714	0.035247	0.02537	0.326347	PDCD2
211385 x at	U28169.1	0.035714	0.035247	0.0891	0.326218	SULT1A2
209019 s at	AF316873.1	0.035714	0.035247	0.022727	0.3257	PINK1
219067 s at	NM 017615.1	0.035714	0.035247	0.087717	0.325056	FLJ20003
201871 s at	NM 015853.1	0.035714	0.035247	0.021537	0.321089	LOC51035
219192 at	NM 018449.1	0.035714	0.035247	0.01461	0.318475	UBAP2
204978 at	NM 007056.1	0.035714	0.035247	0.013827	0.318086	SWAP2
215691 x at	AV702994	0.035714	0.035247	0.010766	0.316138	LOC51668
215090 x at	AK021884.1	0.035714	0.04225	0.016862	0.315879	NPEPPS
208709 s at	U64898.1	0.035714	0.035247	0.012705	0.309446	NRD1



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44617 at	AI431902	0.035714	0.035247	0.026163	0.307321	FLJ13491
202139 at	NM 003689.1	0.035714	0.04225	0.03366	0.306281	AKR7A2
203289 s at	BE791629	0.035714	0.00747	0.039522	0.304821	CGTHBA
204000 at	NM 016194.1	0.035714	0.035247	0.060249	0.303474	GNB5
202080 s at	NM 014965.1	0.035714	0.035247	0.013547	0.298042	KIAA1042
202682 s at	NM 003363.1	0.035714	0.035247	0.018393	0.295239	USP4
33304 at	U88964	0.035714	0.035247	0.019349	0.294427	ISG20
209729 at	BC001782.1	0.035714	0.035247	0.059026	0.293156	GAS2L1
209158 s at	BC004361.1	0.035714	0.04225	0.084538	0.292509	PSCD2
217980 s at	NM 017840.1	0.035714	0.035247	0.003929	0.290472	MRPL16
201230 s at	NM 006321.1	0.035714	0.015406	0.006688	0.288723	ARIH2
64486 at	AI341234	0.035714	0.035247	0.007356	0.284699	CORO1B
212486 s at	N20923	0.035714	0.035247	0.020271	0.280552	FYN
211630 s at	L42531.1	0.035714	0.035247	0.008554	0.280023	
214749 s at	AK000818.1	0.035714	0.035247	0.02226	0.277695	FLJ20811
203685 at	NM 000633.1	0.035714	0.035247	0.044639	0.276897	BCL2
213607 x at	BE551347	0.035714	0.035247	0.209003	0.276406	FLJ13052
202808 at	AK000161.1	0.035714	0.04225	0.016752	0.276103	FLJ20154
212735 at	AI798908	0.035714	0.04225	0.015969	0.274921	KIAA0226
219767 s at	NM 005111.1	0.035714	0.035247	0.01405	0.273732	CRYZL1
201346 at	NM 024551.1	0.035714	0.035247	0.00372	0.272684	FLJ21432
221708 s at	BC006214.1	0.035714	0.00747	0.006244	0.268704	IRO039700
203492 x at	AI123527	0.035714	0.04225	0.105392	0.268349	KIAA0092
204313 s at	NM 004379.1	0.035714	0.035247	0.047229	0.267796	CREB1
213061 s at	AA643304	0.035714	0.035247	0.039678	0.258201	
204744 s at	NM 013417.1	0.035714	0.035247	0.047087	0.257738	IARS
212946 at	AK025432.1	0.035714	0.035247	0.051871	0.257456	KIAA0564
40829 at	AB028960	0.035714	0.04225	0.040942	0.254827	KIAA1037
204608 at	NM 000048.1	0.035714	0.04225	0.038931	0.254447	ASL
200830 at	NM 002808.1	0.035714	0.035247	0.023966	0.250129	PSMD2
207122 x at	NM 001054.1	0.035714	0.035247	0.062598	0.248696	SULT1A2
206219 s at	NM 005428.2	0.035714	0.035247	0.007185	0.248439	VAV1
217925 s at	NM 022758.1	0.035714	0.04225	0.011489	0.246401	FLJ22195
209075 s at	AY009128.1	0.035714	0.035247	0.084938	0.246257	NIFU
214756 x at	AB017004.1	0.035714	0.035247	0.079567	0.244954	PMS2L8
202520 s at	NM 000249.1	0.035714	0.04225	0.021274	0.243441	MLH1
211609 x at	U51007.1	0.035714	0.035247	0.042753	0.242223	
210312 s at	BC002640.1	0.035714	0.035247	0.074751	0.240603	
200861 at	NM 016284.1	0.035714	0.00747	0.001929	0.240076	KIAA1007
201029 s at	NM 002414.1	0.035714	0.035247	0.063998	0.239013	MIC2
210620 s at	BC000212.1	0.035714	0.035247	0.021052	0.237577	GTF3C2
204977 at	NM 004398.2	0.035714	0.035247	0.040656	0.235252	DDX10
218791 s at	NM 024713.1	0.035714	0.035247	0.048887	0.234927	FLJ22557
200882 s at	NM 002810.1	0.035714	0.035247	0.038558	0.234593	PSMD4
219801 at	NM 030580.1	0.035714	0.035247	0.031263	0.233466	MGC10520
212216 at	AB007896.1	0.035714	0.035247	0.211816	0.231563	KIAA0436

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205192 at	NM 003954.1	0.035714	0.04225	0.051916	0.230862	MAP3K14
205661 s at	NM 025207.1	0.035714	0.035247	0.020823	0.230015	PP591
219863 at	NM 016323.1	0.035714	0.035247	0.051393	0.228764	LOC51191
218969 at	NM 016069.1	0.035714	0.04225	0.132766	0.223618	Magmas
218407 x at	NM 013349.1	0.035714	0.035247	0.028748	0.223073	SPUF
201892 s at	NM 000884.1	0.035714	0.035247	0.064347	0.222421	IMPDH2
222264 at	BG167570	0.035714	0.04225	0.108243	0.219652	DKFZp762N1910
201740 at	NM 004551.1	0.035714	0.00747	0.06025	0.217427	NDUFS3
200742 s at	BG231932	0.035714	0.04225	0.079649	0.210447	CLN2
219034 at	NM 017851.1	0.035714	0.035247	0.036308	0.209956	FLJ20509
201999 s at	NM 006519.1	0.035714	0.035247	0.032991	0.202387	TCTEL1
209746 s at	AF032900.1	0.035714	0.035247	0.174549	0.200739	COQ7
200920 s at	AL535380	0.035714	0.035247	0.265205	0.198073	BTG1
203704 s at	AW118862	0.035714	0.035247	0.02173	0.193753	RREB1
202054 s at	NM 000382.1	0.035714	0.035247	0.27948	0.193509	ALDH3A2
219394 at	NM 024419.1	0.035714	0.035247	0.164883	0.190623	PGS1
200054 at	NM 003904.1	0.035714	0.035247	0.245676	0.190422	ZNF259
209971 x at	AI928526	0.035714	0.00747	0.036861	0.185624	JTV1
220150 s at	NM 024581.1	0.035714	0.035247	0.230867	0.185323	FLJ13942
208749 x at	AF085357.1	0.035714	0.035247	0.110175	0.184965	FLOT1
201350 at	NM 004475.1	0.035714	0.035247	0.072642	0.180483	FLOT2
221699 s at	AF334103.1	0.035714	0.00747	0.009664	0.17511	GU2
218592 s at	NM 017829.1	0.035714	0.035247	0.110207	0.174515	CECR5
202041 s at	NM 004214.3	0.035714	0.04225	0.016835	0.157902	FIBP
219069 at	NM 017704.1	0.035714	0.04225	0.16159	0.157672	FLJ20189
207614 s at	NM 003592.1	0.035714	0.035247	0.038652	0.146241	CUL1
201060 x at	AI537887	0.035714	0.035247	0.467375	0.139355	EPB72
218159 at	NM 023935.1	0.035714	0.035247	0.049119	0.125305	C20orf116
201528 at	BG398414	0.035714	0.035247	0.286856	0.123085	RPA1
202263 at	NM 016243.1	0.035714	0.035247	0.279995	0.121894	LOC51706
218287 s at	NM 012199.1	0.035714	0.035247	0.093241	0.118547	EIF2C1
212508 at	AK024029.1	0.035714	0.04225	0.450393	0.11646	MAP-1
207571 x at	NM 004848.1	0.035714	0.035247	0.486492	0.113516	ICB-1
212322 at	AF144638.1	0.035714	0.035247	0.255571	0.10089	SGPL1
210667 s at	D86062.1	0.035714	0.035247	0.532398	0.084417	C21orf33
204563 at	NM 000655.2	0.035714	0.035247	0.535745	0.081167	SELL
219434 at	NM 018643.1	0.035714	0.035247	0.870775	0.057399	TREM1
219243 at	NM 018326.1	0.035714	0.035247	0.929375	0.035048	HIMAP4
204027 s at	NM 005371.2	0.035714	0.035247	0.876737	0.025127	METTL1
201281 at	NM 007002.1	0.035714	0.035247	0.911541	0.010422	ADRM1
207629 s at	NM 004723.1	0.035714	0.035247	0.975685	-0.00562	ARHGEF2
35265 at	U31501	0.035714	0.035247	0.724549	-0.0658	FXR2
205425 at	NM 005338.3	0.035714	0.04225	0.126911	-0.0661	HIP1
210780 at	AB006589.1	0.035714	0.035247	0.00542	-0.10655	ESR2
212569 at	AA868754	0.035714	0.035247	0.304519	-0.10746	KIAA0650
215671 at	AU144792	0.035714	0.035247	0.008623	-0.11362	

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214629	x at	AF320999.1	0.035714	0.035247	0.289096	-0.11449	RTN4
204859	s at	NM 013229.1	0.035714	0.035247	0.529181	-0.13735	APAF1
220023	at	NM 018690.1	0.035714	0.04225	0.261146	-0.14482	APOB48R
213012	at	D42055.1	0.035714	0.04225	0.007978	-0.14841	NEDD4
212696	s at	BF968633	0.035714	0.035247	0.135003	-0.14873	RNF4
209022	at	AK026678.1	0.035714	0.035247	0.00833	-0.15056	STAG2
201817	at	NM 014671.1	0.035714	0.035247	0.392979	-0.15386	KIAA0010
208113	x at	NM 030979.1	0.035714	0.035247	0.087494	-0.15652	PABPC3
215022	x at	BG429214	0.035714	0.035247	0.273519	-0.15766	
220668	s at	NM 006892.1	0.035714	0.035247	0.001922	-0.15828	DNMT3B
201174	s at	NM 018975.1	0.035714	0.035247	0.042202	-0.16723	RAP1
200994	at	AL137335.1	0.035714	0.035247	0.306422	-0.17292	RANBP7
202797	at	NM 014016.1	0.035714	0.035247	0.398036	-0.17365	SACM1L
203765	at	NM 012198.1	0.035714	0.035247	0.391555	-0.17556	GCA
218047	at	NM 024586.1	0.035714	0.04225	0.011965	-0.19298	OSBPL9
201964	at	N64643	0.035714	0.035247	0.16498	-0.19313	KIAA0625
206461	x at	NM 005951.1	0.035714	0.035247	0.156965	-0.1942	MT1H
202055	at	NM 002264.1	0.035714	0.035247	0.138195	-0.1949	
217856	at	AF182415.1	0.035714	0.04225	0.325959	-0.19495	RBM8A
214225	at	BE674061	0.035714	0.035247	0.015036	-0.20133	PIN4
203298	s at	NM 004973.2	0.035714	0.00747	0.103071	-0.20162	JMJ
211584	s at	U58852.1	0.035714	0.035247	0.510508	-0.20606	NPAT
205270	s at	NM 005565.2	0.035714	0.035247	0.037541	-0.2105	LCP2
203334	at	NM 004941.1	0.035714	0.035247	0.229189	-0.21215	DDX8
209880	s at	U02297.1	0.035714	0.035247	0.252672	-0.21782	SELPLG
201873	s at	NM 002940.1	0.035714	0.035247	0.112373	-0.22731	ABCE1
208677	s at	AL550657	0.035714	0.035247	0.069403	-0.23303	BSG
222283	at	BG387770	0.035714	0.035247	0.032984	-0.2362	MGC32104
212714	at	AL050205.1	0.035714	0.04225	0.352078	-0.23748	LOC113251
218833	at	NM 016653.1	0.035714	0.035247	0.003387	-0.23765	ZAK
214201	x at	AA742237	0.035714	0.035247	0.120935	-0.23853	BAT2
218669	at	NM 021183.1	0.035714	0.035247	0.069121	-0.24239	LOC57826
212306	at	AB014527.1	0.035714	0.035247	0.005636	-0.24315	CLASP2
213379	at	AF091086.1	0.035714	0.035247	0.124853	-0.24621	CL640
203761	at	NM 006748.1	0.035714	0.04225	0.141473	-0.24728	SLA
217945	at	NM 025238.1	0.035714	0.035247	0.046507	-0.24841	BTBD1
219017	at	NM 018638.2	0.035714	0.035247	0.074405	-0.24942	EKI1
208021	s at	NM 002913.1	0.035714	0.04225	0.092197	-0.24967	
202990	at	NM 002863.1	0.035714	0.035247	0.034567	-0.25494	PYGL
209481	at	AF226044.1	0.035714	0.035247	0.023966	-0.25679	SNRK
218603	at	NM 016217.1	0.035714	0.035247	0.01673	-0.25733	LOC51696
209585	s at	AF084943.1	0.035714	0.035247	0.024841	-0.26011	MINPP1
213044	at	N22548	0.035714	0.04225	0.03686	-0.26164	ROCK1
209643	s at	AF033850.1	0.035714	0.035247	0.110532	-0.26338	PLD2
200971	s at	NM 014445.1	0.035714	0.00747	0.007058	-0.26858	SERP1
205115	s at	NM 016196.1	0.035714	0.035247	0.014278	-0.27109	KIAA0682

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206715 at	NM 012252.1	0.035714	0.035247	0.020625	-0.27124	TFEC
202877 s at	W72082	0.035714	0.035247	0.180599	-0.27284	C1QR1
217863 at	NM 016166.1	0.035714	0.035247	0.071782	-0.27429	PIAS1
219628 at	NM 022470.1	0.035714	0.035247	0.072884	-0.27655	WIG1
208092 s at	NM 030797.1	0.035714	0.035247	0.039197	-0.27728	DKFZP566A1524
203275 at	NM 002199.2	0.035714	0.035247	0.250656	-0.27789	IRF2
208896 at	BC003360.1	0.035714	0.035247	0.02171	-0.27851	DDX18
218092 s at	NM 004504.2	0.035714	0.035247	0.020834	-0.27873	HRB
202878 s at	NM 012072.2	0.035714	0.035247	0.118494	-0.27892	C1QR1
202184 s at	NM 018230.1	0.035714	0.035247	0.071301	-0.28019	NUP133
201859 at	NM 002727.1	0.035714	0.04225	0.038559	-0.28438	PRG1
201238 s at	BC005338.1	0.035714	0.035247	0.114062	-0.28524	CAPZA2
203984 s at	U60521.1	0.035714	0.04225	0.066643	-0.29174	CASP9
206025 s at	AW188198	0.035714	0.035247	0.005126	-0.29178	TNFAIP6
213129 s at	BE908931	0.035714	0.035247	0.017009	-0.29572	
215823 x at	U64661	0.035714	0.04225	0.030982	-0.29704	
217346 at	AL021395	0.035714	0.04225	0.02084	-0.29857	
202272 s at	NM 015176.1	0.035714	0.035247	0.059688	-0.299	KIAA0483
201707 at	NM 002857.1	0.035714	0.04225	0.04761	-0.29944	PXF
209124 at	U70451.1	0.035714	0.035247	0.003458	-0.30169	MYD88
219885 at	NM 018042.1	0.035714	0.035247	0.020209	-0.30409	FLJ10260
212195 at	AL049265.1	0.035714	0.04225	0.136618	-0.30472	
207291 at	NM 024081.1	0.035714	0.035247	0.020267	-0.30513	TMG4
209602 s at	AI796169	0.035714	0.035247	0.023959	-0.31104	GATA3
213291 s at	AA160522	0.035714	0.035247	0.056044	-0.31114	UBE3A
210281 s at	AL136621.1	0.035714	0.04225	0.06859	-0.31538	ZNF198
202236 s at	NM 003051.1	0.035714	0.035247	0.028776	-0.3171	SLC16A1
212286 at	AW572909	0.035714	0.035247	0.027025	-0.31713	KIAA0874
218331 s at	NM 017782.1	0.035714	0.04225	0.017104	-0.32078	FLJ20360
212959 s at	AK001821.1	0.035714	0.04225	0.013182	-0.32145	MGC4170
214875 x at	AW001847	0.035714	0.035247	0.204195	-0.32259	APLP2
203730 s at	BF196931	0.035714	0.04225	0.003706	-0.3226	ZFP95
206308 at	AJ223333.1	0.035714	0.035247	0.023593	-0.32279	DNMT2
204971 at	NM 005213.1	0.035714	0.04225	0.216305	-0.32285	CSTA
212262 at	AF142419.1	0.035714	0.04225	0.013772	-0.33425	QKI
219099 at	NM 020375.1	0.035714	0.035247	0.07666	-0.33473	C12orf5
217971 at	NM 021970.1	0.035714	0.04225	0.054987	-0.33505	MAP2K1IP1
215006 at	AK023816.1	0.035714	0.035247	0.136952	-0.34214	
218878 s at	NM 012238.3	0.035714	0.00747	0.018308	-0.3438	SIRT1
201362 at	AF205218.1	0.035714	0.035247	0.033088	-0.34674	NS1-BP
201097 s at	NM 001660.2	0.035714	0.035247	0.020387	-0.35015	ARF4
204493 at	NM 001196.1	0.035714	0.015406	0.020544	-0.35511	BID
203455 s at	NM 002970.1	0.035714	0.035247	0.064201	-0.35676	SAT
217403 s at	AC074331	0.035714	0.035247	0.01515	-0.35767	
201573 s at	M75715.1	0.035714	0.035247	0.010802	-0.3577	ETF1
218926 at	NM 018657.2	0.035714	0.04225	0.021807	-0.3681	MYNN

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202205	at	NM 003370.1	0.035714	0.035247	0.056143	-0.37617	VASP
202934	at	AI761561	0.035714	0.035247	0.084393	-0.37861	HK2
202925	s at	NM 002657.2	0.035714	0.035247	0.043402	-0.39004	PLAGL2
203503	s at	NM 004565.1	0.035714	0.035247	0.086212	-0.39025	PEX14
212209	at	AK023837.1	0.035714	0.04225	0.083366	-0.39056	KIAA1025
202194	at	AL117354	0.035714	0.00747	0.011916	-0.39754	LOC50999
201210	at	NM 001356.2	0.035714	0.035247	0.029134	-0.41337	DDX3
218041	x at	NM 018573.1	0.035714	0.015406	0.00529	-0.41757	PRO1068
221423	s at	NM 030799.1	0.035714	0.035247	0.075235	-0.42088	SMAP-5
213649	at	AA524053	0.035714	0.04225	0.031361	-0.42442	
207121	s at	NM 002748.1	0.035714	0.035247	0.023266	-0.42563	MAPK6
202270	at	NM 002053.1	0.035714	0.035247	0.053201	-0.43747	GBP1
212838	at	AB023227.1	0.035714	0.04225	0.003343	-0.43985	KIAA1010
202814	s at	AW193511	0.035714	0.035247	0.012709	-0.44652	HIS1
203432	at	AW272611	0.035714	0.04225	0.024277	-0.44899	TMPO
212644	s at	AI671747	0.035714	0.00747	0.02288	-0.45263	MISS
209362	at	AI688580	0.035714	0.035247	0.035918	-0.45484	SURB7
207535	s at	NM 002502.1	0.035714	0.035247	0.107712	-0.45745	NFKB2
203921	at	NM 004267.1	0.035714	0.04225	0.030352	-0.47177	CHST2
216841	s at	X15132.1	0.035714	0.035247	0.041452	-0.47259	SOD2
219308	s at	NM 012093.1	0.035714	0.035247	0.011606	-0.47474	AK5
212623	at	D26067.1	0.035714	0.035247	0.003438	-0.47644	KIAA0033
202076	at	NM 001166.2	0.035714	0.04225	0.015252	-0.48334	BIRC2
218611	at	NM 016545.1	0.035714	0.035247	0.029826	-0.48723	IER5
201963	at	NM 021122.2	0.035714	0.035247	0.070882	-0.49855	FACL2
220369	at	NM 017936.1	0.035714	0.035247	0.008293	-0.5016	FLJ20707
201925	s at	NM 000574.1	0.035714	0.035247	0.022743	-0.50532	DAF
212749	s at	AL050144.1	0.035714	0.015406	0.000822	-0.52839	ZNF363
202581	at	NM 005346.2	0.035714	0.035247	0.10824	-0.5359	HSPA1B
218689	at	NM 022725.1	0.035714	0.035247	0.023814	-0.53779	FANCF
200962	at	AI348010	0.035714	0.035247	0.226116	-0.54348	
201799	s at	AI927993	0.035714	0.035247	0.054067	-0.54478	OSBP
213281	at	BE327172	0.035714	0.035247	0.091317	-0.54925	JUN
213021	at	AI741876	0.035714	0.00747	0.025182	-0.57505	
201416	at	NM 003107.1	0.035714	0.035247	0.078087	-0.59709	SOX4
216300	x at	BE383139	0.035714	0.035247	0.00951	-0.60058	RARA
219714	s at	NM 018398.1	0.035714	0.035247	0.016221	-0.603	CACNA2D3
202638	s at	NM 000201.1	0.035714	0.035247	0.036915	-0.62554	ICAM1
201473	at	NM 002229.1	0.035714	0.035247	0.129802	-0.64436	JUNB
200798	x at	NM 021960.1	0.035714	0.04225	0.024176	-0.66914	MCL1
205308	at	NM 016010.1	0.035714	0.00747	0.015684	-0.68307	LOC51101
201041	s at	NM 004417.2	0.035714	0.035247	0.043377	-0.68458	DUSP1
202241	at	NM 025195.1	0.035714	0.035247	0.055882	-0.68638	C8FW
204794	at	NM 004418.2	0.035714	0.035247	0.306591	-0.68934	DUSP2
208961	s at	AB017493.1	0.035714	0.015406	0.010224	-0.6982	COPEB
209545	s at	AF064824.1	0.035714	0.035247	0.010071	-0.70109	RIPK2

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203751	x at	NM 005354.2	0.035714	0.035247	0.04394	-0.70667	JUND
206245	s at	NM 006469.1	0.035714	0.035247	0.006453	-0.71493	NS1-BP
202644	s at	NM 006290.1	0.035714	0.035247	0.155375	-0.73437	TNFAIP3
214326	x at	AI339541	0.035714	0.035247	0.039838	-0.76402	JUND
209304	x at	AF087853.1	0.035714	0.035247	0.076647	-0.77217	GADD45B
216336	x at	AL031602	0.035714	0.035247	0.015158	-0.78504	
221477	s at	BF575213	0.035714	0.035247	0.007144	-0.78651	
201670	s at	M68956.1	0.035714	0.00747	0.001933	-0.79718	MARCKS
202081	at	NM 004907.1	0.035714	0.035247	0.006503	-0.81053	ETR101
212659	s at	AW083357	0.035714	0.035247	0.009893	-0.81405	IL1RN
206765	at	AF153820.1	0.035714	0.035247	0.004403	-0.82757	KCNJ2
202637	s at	AI608725	0.035714	0.035247	0.010119	-0.83319	ICAM1
204897	at	NM 000958.1	0.035714	0.015406	0.003112	-0.86354	PTGER4
214211	at	AA083483	0.035714	0.035247	0.012228	-0.88452	FTH1
203471	s at	NM 002664.1	0.035714	0.00747	0.000855	-0.88664	PLEK
213038	at	AL031602	0.035714	0.015406	0.00038	-0.88673	
36564	at	W27419	0.035714	0.015406	0.000361	-0.95575	
206157	at	NM 002852.1	0.035714	0.035247	0.001716	-0.97365	PTX3
201694	s at	NM 001964.1	0.035714	0.035247	0.068287	-0.99045	EGR1
209305	s at	AF078077.1	0.035714	0.035247	0.017058	-1.003	GADD45B
213524	s at	NM 015714.1	0.035714	0.035247	0.210858	-1.05996	G0S2
209189	at	BC004490.1	0.035714	0.035247	0.068201	-1.06388	FOS
202643	s at	AI738896	0.035714	0.035247	0.071526	-1.09453	TNFAIP3
222326	at	AW973834	0.035714	0.035247	0.030817	-1.09468	
207075	at	NM 004895.1	0.035714	0.035247	0.004992	-1.10724	CIAS1
210845	s at	U08839.1	0.035714	0.035247	0.030968	-1.1245	PLAUR
201489	at	BC005020.1	0.035714	0.035247	0.022893	-1.13801	PPIF
201739	at	NM 005627.1	0.035714	0.035247	0.010834	-1.16132	SGK
207574	s at	NM 015675.1	0.035714	0.035247	0.022251	-1.16822	GADD45B
203470	s at	AI433595	0.035714	0.015406	0.002395	-1.17663	PLEK
202340	x at	NM 002135.1	0.035714	0.035247	0.009942	-1.19934	NR4A1
201531	at	NM 003407.1	0.035714	0.035247	0.0028	-1.30448	ZFP36
204440	at	NM 004233.1	0.035714	0.035247	0.045128	-1.33091	CD83
205767	at	NM 001432.1	0.035714	0.035247	0.001942	-1.33633	EREG
201466	s at	NM 002228.2	0.035714	0.035247	0.007227	-1.34352	JUN
205681	at	NM 004049.1	0.035714	0.035247	0.004927	-1.41895	BCL2A1
37028	at	U83981	0.035714	0.035247	0.005806	-1.46885	PPP1R15A
205220	at	NM 006018.1	0.035714	0.035247	0.002094	-1.50671	HM74
201464	x at	BG491844	0.035714	0.035247	0.011957	-1.61438	JUN
201465	s at	BC002646.1	0.035714	0.035247	0.002438	-1.64136	JUN
204748	at	NM 000963.1	0.035714	0.035247	0.025772	-1.65759	PTGS2
211924	s at	AY029180.1	0.035714	0.035247	0.011082	-1.69399	PLAUR
202014	at	NM 014330.2	0.035714	0.035247	0.003245	-1.74665	PPP1R15A
201631	s at	NM 003897.1	0.035714	0.035247	0.002981	-1.89968	IER3
209774	x at	M57731.1	0.035714	0.035247	0.001811	-1.9703	CXCL2
202859	x at	NM 000584.1	0.035714	0.035247	0.030747	-2.54298	IL8

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205067 at	NM_000576.1	0.035714	0.035247	0.000992	-2.66025	IL1B
39402 at	M15330	0.035714	0.035247	0.001505	-2.71142	IL1B

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination.

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims. All publications, patents, patent applications and sequences identified by a GenBank accession number mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent, patent application or sequence was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention.